

gca gag agt agc cag gac ctc gag ttc cag tgg ctg aga gaa gag aca 1153
 Ala Glu Ser Ser Gln Asp Leu Glu Phe Gln Trp Leu Arg Glu Glu Thr
 370 375 380
 gac cag gtg ctg gaa agg ggg cct gtg ctt cag ttg cat gac ctg aaa 1201
 Asp Gln Val Leu Glu Arg Gly Pro Val Leu Gln Leu His Asp Leu Lys
 385 390 395
 cgg gag gca gga ggc ggc tat cgc tgc gtg gcg tct gtg ccc agc ata 1249
 Arg Glu Ala Gly Gly Gly Tyr Arg Cys Val Ala Ser Val Pro Ser Ile
 400 405 410
 ccc ggc ctg aac cgc aca cag ctg gtc aag ctg gcc att ttt ggc ccc 1297
 Pro Gly Leu Asn Arg Thr Gln Leu Val Lys Leu Ala Ile Phe Gly Pro
 415 420 425 430
 cct tgg atg gca ttc aag gag agg aag gtg tgg gtg aaa gag aat atg 1345
 Pro Trp Met Ala Phe Lys Glu Arg Lys Val Trp Val Lys Glu Asn Met
 435 440 445
 gtg ttg aat ctg tct tgt gaa gcg tca ggg cac ccc cgg ccc acc atc 1393
 Val Leu Asn Leu Ser Cys Glu Ala Ser Gly His Pro Arg Pro Thr Ile
 450 455 460
 tcc tgg aac gtc aac ggc acg gca agt gaa caa gac caa gat cca cag 1441
 Ser Trp Asn Val Asn Gly Thr Ala Ser Glu Gln Asp Gln Asp Pro Gln
 465 470 475
 cga gtc ctg agc acc ctg aat gtc ctc gtg acc ccg gag ctg ttg gag 1489
 Arg Val Leu Ser Thr Leu Asn Val Leu Val Thr Pro Glu Leu Leu Glu
 480 485 490
 aca ggt gtt gaa tgc acg gcc tcc aac gac ctg ggc aaa aac acc agc 1537
 Thr Gly Val Glu Cys Thr Ala Ser Asn Asp Leu Gly Lys Asn Thr Ser

495	500	505	510	
atc ctc ttc ctg gag ctg gtc aat tta acc acc ctc aca cca gac tcc				1585
Ile Leu Phe Leu Glu Leu Val Asn Leu Thr Thr Leu Thr Pro Asp Ser				
	515	520	525	
aac aca acc act ggc ctc agc act tcc act gcc agt cct cat acc aga				1633
Asn Thr Thr Thr Gly Leu Ser Thr Ser Thr Ala Ser Pro His Thr Arg				
	530	535	540	
gcc aac agc acc tcc aca gag aga aag ctg ccg gag ccg gag agc cgg				1681
Ala Asn Ser Thr Ser Thr Glu Arg Lys Leu Pro Glu Pro Glu Ser Arg				
	545	550	555	
ggc gtg gtc atc gtg gct gtg att gtg tgc atc ctg gtc ctg gcg gtg				1729
Gly Val Val Ile Val Ala Val Ile Val Cys Ile Leu Val Leu Ala Val				
	560	565	570	
ctg ggc gct gtc ctc tat ttc ctc tat aag aag ggc aag ctg ccg tgc				1777
Leu Gly Ala Val Leu Tyr Phe Leu Tyr Lys Lys Gly Lys Leu Pro Cys				
575	580	585	590	
agg cgc tca ggg aag cag gag atc acg ctg ccc ccg tct cgt aag acc				1825
Arg Arg Ser Gly Lys Gln Glu Ile Thr Leu Pro Pro Ser Arg Lys Thr				
	595	600	605	
gaa ctt gla gtt gaa gtt aag tca gat aag ctc cca gaa gag atg ggc				1873
Glu Leu Val Val Glu Val Lys Ser Asp Lys Leu Pro Glu Glu Met Gly				
	610	615	620	
ctc ctg cag ggc agc agc ggt gac aag agg gct ccg gga gac cag gga				1921
Leu Leu Gln Gly Ser Ser Gly Asp Lys Arg Ala Pro Gly Asp Gln Gly				
	625	630	635	
gag aaa tac atc gat ctg agg cat tagccccgaa tcacttcagc tcccttcct				1975
Glu Lys Tyr Ile Asp Leu Arg His				

640

645

gccitggacca ttcccagctc cctgcicact cttctctcag ccaaagctca aagggactag 2035
 agagaagcct ccigctcccc tgcctigcac acccccttc agagggccac tgggttagga 2095
 cctgaggacc tcacttgccc ctgcaaggcc cgcctttcag ggaccagtcc accaccatct 2155
 cctccacgtt gagtgaagct cateccaagc aaggagcccc agtctccga ggggtagga 2215
 gagtttcttg cagaacgtgt ttttcttta cacacattat gcigttaaata cgctcgtcct 2275
 gccagcagct gagctgggta gcctctctga gctggtttcc tgcccaaag gctggcattc 2335
 caccatccag gtcaccact gaagttagga cacaccggag ccaggcgcct gctcatgttg 2395
 aagtgcgtg ttacaccccg ctccggagag caccacagca gcatccagaa gcagctgcag 2455
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 cacaaagica gacgagacca tcttgctaa cacgtgaaa cctgtctct actaaaaata 2695
 caaaaaaaaa ttagctaggc gtagtggttg gcacclatag tcccagctac tcggaaggct 2755
 gaagcaggag aatggtatga atccaggagg tggagcttgc agtgagccga gaccgtgcca 2815
 ctgcactcca gcctgggcaa cacagcgaga ctccgtctcg aggaaaaaaaa aaatcgtgct 2875
 cgtagcagct ggctctgttt cgagtcaggt gaattagcct caatccccgt gttcacttgc 2935
 tcccatagcc ctcttgatgg atcacgtaaa actgaaaggc agcggggagc agacaaagat 2995
 gaggtctaca ctgtccitca tggggattaa agctatggtt atattagcac caaacttcta 3055
 caaaccaagc tcaggaccca accctagaag ggcccaaatg agagaatggt acttaggat 3115
 ggcaaacgg gcctggctag agcttcgggt gtgtgtgtct gtctgtgtat gcatacalat 3175
 gtgtgtatat atggttttgt cagggtgtga aatttgcaa ttgtttcctt tatatatgta 3235
 tgtatatata tatatgaaa tatatatata tatgaaaaat aaagcttaat tgtcccag 3293

<210> 96

<211> 646

<212> PRT

<213> Homo sapiens

<400> 96

Met Gly Leu Pro Arg Leu Val Cys Ala Phe Leu Leu Ala Ala Cys Cys

1 5 10 15

Cys Cys Pro Arg Val Ala Gly Val Pro Gly Glu Ala Glu Gln Pro Ala

20 25 30

Pro Glu Leu Val Glu Val Glu Val Gly Ser Thr Ala Leu Leu Lys Cys

35 40 45

Gly Leu Ser Gln Ser Gln Gly Asn Leu Ser His Val Asp Trp Phe Ser

50 55 60

Val His Lys Glu Lys Arg Thr Leu Ile Phe Arg Val Arg Gln Gly Gln

65 70 75 80

Gly Gln Ser Glu Pro Gly Glu Tyr Glu Gln Arg Leu Ser Leu Gln Asp

85 90 95

Arg Gly Ala Thr Leu Ala Leu Thr Gln Val Thr Pro Gln Asp Glu Arg

100 105 110

Ile Phe Leu Cys Gln Gly Lys Arg Pro Arg Ser Gln Glu Tyr Arg Ile

115 120 125

Gln Leu Arg Val Tyr Lys Ala Pro Glu Glu Pro Asn Ile Gln Val Asn

130 135 140

Pro Leu Gly Ile Pro Val Asn Ser Lys Glu Pro Glu Glu Val Ala Thr

145 150 155 160

Cys Val Gly Arg Asn Gly Tyr Pro Ile Pro Gln Val Ile Trp Tyr Lys

165 170 175

Asn Gly Arg Pro Leu Lys Glu Glu Lys Asn Arg Val His Ile Gln Ser

180 185 190

Ser Gln Thr Val Glu Ser Ser Gly Leu Tyr Thr Leu Gln Ser Ile Leu
 195 200 205
 Lys Ala Gln Leu Val Lys Glu Asp Lys Asp Ala Gln Phe Tyr Cys Glu
 210 215 220
 Leu Asn Tyr Arg Leu Pro Ser Gly Asn His Met Lys Glu Ser Arg Glu
 225 230 235 240
 Val Thr Val Pro Val Phe Tyr Pro Thr Glu Lys Val Trp Leu Glu Val
 245 250 255
 Glu Pro Val Gly Met Leu Lys Glu Gly Asp Arg Val Glu Ile Arg Cys
 260 265 270
 Leu Ala Asp Gly Asn Pro Pro Pro His Phe Ser Ile Ser Lys Gln Asn
 275 280 285
 Pro Ser Thr Arg Glu Ala Glu Glu Glu Thr Thr Asn Asp Asn Gly Val
 290 295 300
 Leu Val Leu Glu Pro Ala Arg Lys Glu His Ser Gly Arg Tyr Glu Cys
 305 310 315 320
 Gln Ala Trp Asn Leu Asp Thr Met Ile Ser Leu Leu Ser Glu Pro Gln
 325 330 335
 Glu Leu Leu Val Asn Tyr Val Ser Asp Val Arg Val Ser Pro Ala Ala
 340 345 350
 Pro Glu Arg Gln Glu Gly Ser Ser Leu Thr Leu Thr Cys Glu Ala Glu
 355 360 365
 Ser Ser Gln Asp Leu Glu Phe Gln Trp Leu Arg Glu Glu Thr Asp Gln
 370 375 380
 Val Leu Glu Arg Gly Pro Val Leu Gln Leu His Asp Leu Lys Arg Glu
 385 390 395 400
 Ala Gly Gly Gly Tyr Arg Cys Val Ala Ser Val Pro Ser Ile Pro Gly

405	410	415	
Leu Asn Arg Thr Gln Leu Val Lys Leu Ala Ile Phe Gly Pro Pro Trp			
420	425	430	
Met Ala Phe Lys Glu Arg Lys Val Trp Val Lys Glu Asn Met Val Leu			
435	440	445	
Asn Leu Ser Cys Glu Ala Ser Gly His Pro Arg Pro Thr Ile Ser Trp			
450	455	460	
Asn Val Asn Gly Thr Ala Ser Glu Gln Asp Gln Asp Pro Gln Arg Val			
465	470	475	480
Leu Ser Thr Leu Asn Val Leu Val Thr Pro Glu Leu Leu Glu Thr Gly			
485	490	495	
Val Glu Cys Thr Ala Ser Asn Asp Leu Gly Lys Asn Thr Ser Ile Leu			
500	505	510	
Phe Leu Glu Leu Val Asn Leu Thr Thr Leu Thr Pro Asp Ser Asn Thr			
515	520	525	
Thr Thr Gly Leu Ser Thr Ser Thr Ala Ser Pro His Thr Arg Ala Asn			
530	535	540	
Ser Thr Ser Thr Glu Arg Lys Leu Pro Glu Pro Glu Ser Arg Gly Val			
545	550	555	560
Val Ile Val Ala Val Ile Val Cys Ile Leu Val Leu Ala Val Leu Gly			
565	570	575	
Ala Val Leu Tyr Phe Leu Tyr Lys Lys Gly Lys Leu Pro Cys Arg Arg			
580	585	590	
Ser Gly Lys Gln Glu Ile Thr Leu Pro Pro Ser Arg Lys Thr Glu Leu			
595	600	605	
Val Val Glu Val Lys Ser Asp Lys Leu Pro Glu Glu Met Gly Leu Leu			

610

615

620

Gln Gly Ser Ser Gly Asp Lys Arg Ala Pro Gly Asp Gln Gly Glu Lys

625

630

635

640

Tyr Ile Asp Leu Arg His

645

<210> 97

<211> 1642

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (158).. (1279)

<400> 97

gaatcggcgg tccgcaggt cccgatggt gcggacagta tgaggcaagc gcagggggac 60
 ggggaccagc agctgtcgcc gccgtctca gggtaagag ggaacagaaa tctttgcccc 120
 ctgactttgg aaatctcggt taacctlcaa actggcg atg tca agg gtt cca agt 175

Met Ser Arg Val Pro Ser

1

5

cct cca cct ccg gca gaa atg tcg agt ggc ccc gta gct gag agt tgg 223

Pro Pro Pro Pro Ala Glu Met Ser Ser Gly Pro Val Ala Glu Ser Trp

10

15

20

tgc tac aca cag atc aag gta gtg aaa ttc tcc tac atg tgg acc atc 271

Cys Tyr Thr Gln Ile Lys Val Val Lys Phe Ser Tyr Met Trp Thr Ile

25

30

35

aat aac ttt agc ttt tgc cgg gag gaa atg ggt gaa gtc att aaa agt 319

Asn Asn Phe Ser Phe Cys Arg Glu Glu Met Gly Glu Val Ile Lys Ser

40	45	50	
tct aca ttt tca tca gga gca aat gat aaa ctg aaa tgg tgt ttg cga	367		
Ser Thr Phe Ser Ser Gly Ala Asn Asp Lys Leu Lys Trp Cys Leu Arg			
55	60	65	70
gta aac ccc aaa ggg tta gat gaa gaa agc aaa gat tac ctg tca ctt	415		
Val Asn Pro Lys Gly Leu Asp Glu Glu Ser Lys Asp Tyr Leu Ser Leu			
75	80	85	
tac ctg tta ctg gtc agc tgt cca aag agt gaa gtt cgg gca aaa ttc	463		
Tyr Leu Leu Leu Val Ser Cys Pro Lys Ser Glu Val Arg Ala Lys Phe			
90	95	100	
aaa ttc tcc atc ctg aat gcc aag gga gaa gaa acc aaa gct atg gag	511		
Lys Phe Ser Ile Leu Asn Ala Lys Gly Glu Glu Thr Lys Ala Met Glu			
105	110	115	
agt caa cgg gca tat agg ttt gtg caa ggc aaa gac tgg gga ttc aag	559		
Ser Gln Arg Ala Tyr Arg Phe Val Gln Gly Lys Asp Trp Gly Phe Lys			
120	125	130	
aaa ttc atc cgt aga gat ttt ctt ttg gat gag gcc aac ggg ctt ctc	607		
Lys Phe Ile Arg Arg Asp Phe Leu Leu Asp Glu Ala Asn Gly Leu Leu			
135	140	145	150
cct gat gac aag ctt acc ctc ttc tgc gag gtg agt gtt gtg caa gat	655		
Pro Asp Asp Lys Leu Thr Leu Phe Cys Glu Val Ser Val Val Gln Asp			
155	160	165	
tct gtc aac att tct ggc cag aat acc atg aac atg gta aag gtt cct	703		
Ser Val Asn Ile Ser Gly Gln Asn Thr Met Asn Met Val Lys Val Pro			
170	175	180	
gag tgc cgg ctg gca gat gag tta gga gga ctg tgg gag aat tcc cgg	751		
Glu Cys Arg Leu Ala Asp Glu Leu Gly Gly Leu Trp Glu Asn Ser Arg			

185	190	195	
ttc aca gac tgc tgc ttg tgt gtt gcc ggc cag gaa ttc cag gct cac 799			
Phe Thr Asp Cys Cys Leu Cys Val Ala Gly Gln Glu Phe Gln Ala His			
200	205	210	
aag gct atc tta gca gct cgt tct ccg gtt ttt agt gcc atg ttt gaa 847			
Lys Ala Ile Leu Ala Ala Arg Ser Pro Val Phe Ser Ala Met Phe Glu			
215	220	225	230
cat gaa atg gag gag agc aaa aag aat cga gtt gaa atc aat gat gtg 895			
His Glu Met Glu Glu Ser Lys Lys Asn Arg Val Glu Ile Asn Asp Val			
235	240	245	
gag cct gaa gtt ttt aag gaa atg atg tgc ttc att tac acg ggg aag 943			
Glu Pro Glu Val Phe Lys Glu Met Met Cys Phe Ile Tyr Thr Gly Lys			
250	255	260	
gct cca aac ctc gac aaa atg gct gat gat ttg ctg gca gct gct gac 991			
Ala Pro Asn Leu Asp Lys Met Ala Asp Asp Leu Leu Ala Ala Ala Asp			
265	270	275	
aag tat gcc ctg gag cgc tta aag gtc atg tgt gag gat gcc ctc tgc 1039			
Lys Tyr Ala Leu Glu Arg Leu Lys Val Met Cys Glu Asp Ala Leu Cys			
280	285	290	
agt aac ctg tcc gtg gag aac gct gca gaa att ctc atc ctg gcc gac 1087			
Ser Asn Leu Ser Val Glu Asn Ala Ala Glu Ile Leu Ile Leu Ala Asp			
295	300	305	310
ctc cac agt gca gat cag ttg aaa act cag gca gtg gat ttc atc aac 1135			
Leu His Ser Ala Asp Gln Leu Lys Thr Gln Ala Val Asp Phe Ile Asn			
315	320	325	
tat cat gct tcg gat gtc ttg gag acc tct ggg tgg aag tca atg gtg 1183			

Tyr His Ala Ser Asp Val Leu Glu Thr Ser Gly Trp Lys Ser Met Val

330

335

340

gtg tca cat ccc cac ttg gtg gct gag gca tac cgc tct ctg gct tca 1231

Val Ser His Pro His Leu Val Ala Glu Ala Tyr Arg Ser Leu Ala Ser

345

350

355

gca cag tgc cct ttt ctg gga ccc cca cgc aaa cgc ctg aag caa tcc 1279

Ala Gln Cys Pro Phe Leu Gly Pro Pro Arg Lys Arg Leu Lys Gln Ser

360

365

370

taagatcctg cttgttgtaa gactccgttt aatttcaga agcagcagcc actgttgctg 1339

ccactgacca ccaggtagac agcgcaatct gaggagcttt tactctgttg tgagggaag 1399

agactgcatt gggcccccag acttttaaaa cagcactaaa taacttgggg gaaacggggg 1459

gagggaaaat gaaatgaaaa cctgttgct gcgtcactgt gtccctttg gcctgtctga 1519

gttgataact gtggggattc agtttaggcg ctggcccag gatataccag cgggtgttact 1579

tggagacac ctgtctgcat ctgactgagc agaacaaatc gtcaggtgcc tggagcaaaa 1639

agg

1642

<210> 98

<211> 374

<212> PRT

<213> Homo sapiens

<400> 98

Met Ser Arg Val Pro Ser Pro Pro Pro Ala Glu Met Ser Ser Gly

1

5

10

15

Pro Val Ala Glu Ser Trp Cys Tyr Thr Gln Ile Lys Val Val Lys Phe

20

25

30

Ser Tyr Met Trp Thr Ile Asn Asn Phe Ser Phe Cys Arg Glu Glu Met

35

40

45

Gly Glu Val Ile Lys Ser Ser Thr Phe Ser Ser Gly Ala Asn Asp Lys
 50 55 60
 Leu Lys Trp Cys Leu Arg Val Asn Pro Lys Gly Leu Asp Glu Glu Ser
 65 70 75 80
 Lys Asp Tyr Leu Ser Leu Tyr Leu Leu Leu Val Ser Cys Pro Lys Ser
 85 90 95
 Glu Val Arg Ala Lys Phe Lys Phe Ser Ile Leu Asn Ala Lys Gly Glu
 100 105 110
 Glu Thr Lys Ala Met Glu Ser Gln Arg Ala Tyr Arg Phe Val Gln Gly
 115 120 125
 Lys Asp Trp Gly Phe Lys Lys Phe Ile Arg Arg Asp Phe Leu Leu Asp
 130 135 140
 Glu Ala Asn Gly Leu Leu Pro Asp Asp Lys Leu Thr Leu Phe Cys Glu
 145 150 155 160
 Val Ser Val Val Gln Asp Ser Val Asn Ile Ser Gly Gln Asn Thr Met
 165 170 175
 Asn Met Val Lys Val Pro Glu Cys Arg Leu Ala Asp Glu Leu Gly Gly
 180 185 190
 Leu Trp Glu Asn Ser Arg Phe Thr Asp Cys Cys Leu Cys Val Ala Gly
 195 200 205
 Gln Glu Phe Gln Ala His Lys Ala Ile Leu Ala Ala Arg Ser Pro Val
 210 215 220
 Phe Ser Ala Met Phe Glu His Glu Met Glu Glu Ser Lys Lys Asn Arg
 225 230 235 240
 Val Glu Ile Asn Asp Val Glu Pro Glu Val Phe Lys Glu Met Met Cys
 245 250 255
 Phe Ile Tyr Thr Gly Lys Ala Pro Asn Leu Asp Lys Met Ala Asp Asp

260 265 270
 Leu Leu Ala Ala Ala Asp Lys Tyr Ala Leu Glu Arg Leu Lys Val Met
 275 280 285
 Cys Glu Asp Ala Leu Cys Ser Asn Leu Ser Val Glu Asn Ala Ala Glu
 290 295 300
 Ile Leu Ile Leu Ala Asp Leu His Ser Ala Asp Gln Leu Lys Thr Gln
 305 310 315 320
 Ala Val Asp Phe Ile Asn Tyr His Ala Ser Asp Val Leu Glu Thr Ser
 325 330 335
 Gly Trp Lys Ser Met Val Val Ser His Pro His Leu Val Ala Glu Ala
 340 345 350
 Tyr Arg Ser Leu Ala Ser Ala Gln Cys Pro Phe Leu Gly Pro Pro Arg
 355 360 365
 Lys Arg Leu Lys Gln Ser
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<210> 99

<211> 5722

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (112).. (3621)

<400> 99

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cgccgcgctc cggtagacac aggatccctg ctgggcacca acagctccac c atg ggg 117

Met Gly

1

ctg gcc tgg gga cta ggc gtc ctg ttc ctg atg cat gtg tgt ggc acc 165

Leu Ala Trp Gly Leu Gly Val Leu Phe Leu Met His Val Cys Gly Thr

5

10

15

aac cgc att cca gag tct ggc gga gac aac agc gtg ttt gac atc ttt 213

Asn Arg Ile Pro Glu Ser Gly Gly Asp Asn Ser Val Phe Asp Ile Phe

20

25

30

gaa ctc acc ggg gcc gcc cgc aag ggg tct ggg cgc cga ctg gtg aag 261

Glu Leu Thr Gly Ala Ala Arg Lys Gly Ser Gly Arg Arg Leu Val Lys

35

40

45

50

ggc ccc gac cct tcc agc cca gct ttc cgc atc gag gat gcc aac ctg 309

Gly Pro Asp Pro Ser Ser Pro Ala Phe Arg Ile Glu Asp Ala Asn Leu

55

60

65

atc ccc cct gtg cct gat gac aag ttc caa gac ctg gtg gat gct gtg 357

Ile Pro Pro Val Pro Asp Asp Lys Phe Gln Asp Leu Val Asp Ala Val

70

75

80

cgg gca gaa aag ggt ttc ctc ctt ctg gca tcc ctg agg cag atg aag 405

Arg Ala Glu Lys Gly Phe Leu Leu Leu Ala Ser Leu Arg Gln Met Lys

85

90

95

aag acc cgg ggc acg ctg ctg gcc ctg gag cgg aaa gac cac tct ggc 453

Lys Thr Arg Gly Thr Leu Leu Ala Leu Glu Arg Lys Asp His Ser Gly

100

105

110

cag gtc ttc agc gtg gtg tcc aat ggc aag gcg ggc acc ctg gac ctc 501

Gln Val Phe Ser Val Val Ser Asn Gly Lys Ala Gly Thr Leu Asp Leu

115

120

125

130

agc ctg acc gtc caa gga aag cag cac gtg gtg tct gtg gaa gaa gct 549

Ser Leu Thr Val Gln Gly Lys Gln His Val Val Ser Val Glu Glu Ala
 135 140 145
 ctc ctg gca acc ggc cag tgg aag agc atc acc ctg ttt gtg cag gaa 597
 Leu Leu Ala Thr Gly Gln Trp Lys Ser Ile Thr Leu Phe Val Gln Glu
 150 155 160
 gac agg gcc cag ctg tac atc gac tgt gaa aag atg gag aat gct gag 645
 Asp Arg Ala Gln Leu Tyr Ile Asp Cys Glu Lys Met Glu Asn Ala Glu
 165 170 175
 ttg gac gtc ccc atc caa agc gtc ttc acc aga gac ctg gcc agc atc 693
 Leu Asp Val Pro Ile Gln Ser Val Phe Thr Arg Asp Leu Ala Ser Ile
 180 185 190
 gcc aga ctc cgc atc gca aag ggg ggc gtc aat gac aat ttc cag ggg 741
 Ala Arg Leu Arg Ile Ala Lys Gly Gly Val Asn Asp Asn Phe Gln Gly
 195 200 205 210
 gtg ctg cag aat gtg agg ttt gtc ttt gga acc aca cca gaa gac atc 789
 Val Leu Gln Asn Val Arg Phe Val Phe Gly Thr Thr Pro Glu Asp Ile
 215 220 225
 ctc agg aac aaa ggc tgc tcc agc tct acc agt gtc ctc ctc acc ctt 837
 Leu Arg Asn Lys Gly Cys Ser Ser Ser Thr Ser Val Leu Leu Thr Leu
 230 235 240
 gac aac aac gtg gtg aat ggt tcc agc cct gcc atc cgc act aac tac 885
 Asp Asn Asn Val Val Asn Gly Ser Ser Pro Ala Ile Arg Thr Asn Tyr
 245 250 255
 att ggc cac aag aca aag gac ttg caa gcc atc tgc ggc atc tcc tgt 933
 Ile Gly His Lys Thr Lys Asp Leu Gln Ala Ile Cys Gly Ile Ser Cys
 260 265 270
 gat gag ctg tcc agc atg gtc ctg gaa ctc agg ggc ctg cgc acc att 981

Asp Glu Leu Ser Ser Met Val Leu Glu Leu Arg Gly Leu Arg Thr Ile
 275 280 285 290
 gtg acc acg ctg cag gac agc atc cgc aaa gtg act gaa gag aac aaa 1029
 Val Thr Thr Leu Gln Asp Ser Ile Arg Lys Val Thr Glu Glu Asn Lys
 295 300 305
 gag ttg gcc aat gag ctg agg cgg cct ccc cta tgc tat cac aac gga 1077
 Glu Leu Ala Asn Glu Leu Arg Arg Pro Pro Leu Cys Tyr His Asn Gly
 310 315 320
 gtt cag tac aga aat aac gag gaa tgg act gtt gat agc tgc act gag 1125
 Val Gln Tyr Arg Asn Asn Glu Glu Trp Thr Val Asp Ser Cys Thr Glu
 325 330 335
 tgt cac tgt cag aac tca gtt acc atc tgc aaa aag gtg tcc tgc ccc 1173
 Cys His Cys Gln Asn Ser Val Thr Ile Cys Lys Lys Val Ser Cys Pro
 340 345 350
 atc atg ccc tgc tcc aat gcc aca gtt cct gat gga gaa tgc tgt cct 1221
 Ile Met Pro Cys Ser Asn Ala Thr Val Pro Asp Gly Glu Cys Cys Pro
 355 360 365 370
 cgc tgt tgg ccc agc gac tct gcg gac gat ggc tgg tct cca tgg tcc 1269
 Arg Cys Trp Pro Ser Asp Ser Ala Asp Asp Gly Trp Ser Pro Trp Ser
 375 380 385
 gag tgg acc tcc tgt tct acg agc tgt ggc aat gga att cag cag cgc 1317
 Glu Trp Thr Ser Cys Ser Thr Ser Cys Gly Asn Gly Ile Gln Gln Arg
 390 395 400
 ggc cgc tcc tgc gat agc ctc aac aac cga tgt gag ggc tcc tgc gtc 1365
 Gly Arg Ser Cys Asp Ser Leu Asn Asn Arg Cys Glu Gly Ser Ser Val
 405 410 415

cag aca cgg acc tgc cac att cag gag tgt gac aaa aga ttt aaa cag 1413
 Gln Thr Arg Thr Cys His Ile Gln Glu Cys Asp Lys Arg Phe Lys Gln
 420 425 430
 gat ggt ggc tgg agc cac tgg tcc ccg tgg tca tct tgt tct gtg aca 1461
 Asp Gly Gly Trp Ser His Trp Ser Pro Trp Ser Ser Cys Ser Val Thr
 435 440 445 450
 tgt ggt gat ggt gtg atc aca agg atc cgg ctc tgc aac tct ccc agc 1509
 Cys Gly Asp Gly Val Ile Thr Arg Ile Arg Leu Cys Asn Ser Pro Ser
 455 460 465
 ccc cag atg aat ggg aaa ccc tgt gaa ggc gaa gcg cgg gag acc aaa 1557
 Pro Gln Met Asn Gly Lys Pro Cys Glu Gly Glu Ala Arg Glu Thr Lys
 470 475 480
 gcc tgc aag aaa gac gcc tgc ccc atc aat gga ggc tgg ggt cct tgg 1605
 Ala Cys Lys Lys Asp Ala Cys Pro Ile Asn Gly Gly Trp Gly Pro Trp
 485 490 495
 tca cca tgg gac atc tgt tct gtc acc tgt gga gga ggg gta cag aaa 1653
 Ser Pro Trp Asp Ile Cys Ser Val Thr Cys Gly Gly Gly Val Gln Lys
 500 505 510
 cgt agt cgt ctc tgc aac aac ccc gca ccc cag ttt gga ggc aag gac 1701
 Arg Ser Arg Leu Cys Asn Asn Pro Ala Pro Gln Phe Gly Gly Lys Asp
 515 520 525 530
 tgc gtt ggt gat gta aca gaa aac cag atc tgc aac aag cag gac tgt 1749
 Cys Val Gly Asp Val Thr Glu Asn Gln Ile Cys Asn Lys Gln Asp Cys
 535 540 545
 cca att gat gga tgc ctg tcc aat ccc tgc ttt gcc ggc gtg aag tgt 1797
 Pro Ile Asp Gly Cys Leu Ser Asn Pro Cys Phe Ala Gly Val Lys Cys
 550 555 560

act agc tac cct gat ggc agc tgg aaa tgt ggt gct tgt ccc cct ggt 1845
 Thr Ser Tyr Pro Asp Gly Ser Trp Lys Cys Gly Ala Cys Pro Pro Gly
 565 570 575
 tac agt gga aat ggc atc cag tgc aca gat gtt gat gag tgc aaa gaa 1893
 Tyr Ser Gly Asn Gly Ile Gln Cys Thr Asp Val Asp Glu Cys Lys Glu
 580 585 590
 gtg cct gat gcc tgc ttc aac cac aat gga gag cac cgg tgt gag aac 1941
 Val Pro Asp Ala Cys Phe Asn His Asn Gly Glu His Arg Cys Glu Asn
 595 600 605 610
 acg gac ccc ggc tac aac tgc ctg ccc tgc ccc cca cgc ttc acc ggc 1989
 Thr Asp Pro Gly Tyr Asn Cys Leu Pro Cys Pro Pro Arg Phe Thr Gly
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 tca cag ccc ttc ggc cag ggt gtc gaa cat gcc acg gcc aac aaa cag 2037
 Ser Gln Pro Phe Gly Gln Gly Val Glu His Ala Thr Ala Asn Lys Gln
 630 635 640
 gtg tgc aag ccc cgt aac ccc tgc acg gat ggg acc cac gac tgc aac 2085
 Val Cys Lys Pro Arg Asn Pro Cys Thr Asp Gly Thr His Asp Cys Asn
 645 650 655
 aag aac gcc aag tgc aac tac ctg ggc cac tat agc gac ccc atg tac 2133
 Lys Asn Ala Lys Cys Asn Tyr Leu Gly His Tyr Ser Asp Pro Met Tyr
 660 665 670
 cgc tgc gag tgc aag cct ggc tac gct ggc aat ggc atc atc tgc ggg 2181
 Arg Cys Glu Cys Lys Pro Gly Tyr Ala Gly Asn Gly Ile Ile Cys Gly
 675 680 685 690
 gag gac aca gac ctg gat ggc tgg ccc aat gag aac ctg gtg tgc gtg 2229
 Glu Asp Thr Asp Leu Asp Gly Trp Pro Asn Glu Asn Leu Val Cys Val

695	700	705	
gcc aat gcg act tac cac tgc aaa aag gat aat tgc ccc aac ctt ccc			2277
Ala Asn Ala Thr Tyr His Cys Lys Lys Asp Asn Cys Pro Asn Leu Pro			
710	715	720	
aac tca ggg cag gaa gac tat gac aag gat gga att ggt gat gcc tgt			2325
Asn Ser Gly Gln Glu Asp Tyr Asp Lys Asp Gly Ile Gly Asp Ala Cys			
725	730	735	
gat gat gac gat gac aat gat aaa att cca gat gac agg gac aac tgt			2373
Asp Asp Asp Asp Asp Asn Asp Lys Ile Pro Asp Asp Arg Asp Asn Cys			
740	745	750	
cca ttc cat tac aac cca gct cag tat gac tat gac aga gat gat gtg			2421
Pro Phe His Tyr Asn Pro Ala Gln Tyr Asp Tyr Asp Arg Asp Asp Val			
755	760	765	770
gga gac cgc tgt gac aac tgt ccc tac aac cac aac cca gat cag gca			2469
Gly Asp Arg Cys Asp Asn Cys Pro Tyr Asn His Asn Pro Asp Gln Ala			
775	780	785	
gac aca gac aac aat ggg gaa gga gac gcc tgt gct gca gac att gat			2517
Asp Thr Asp Asn Asn Gly Glu Gly Asp Ala Cys Ala Ala Asp Ile Asp			
790	795	800	
gga gac ggt atc ctc aat gaa cgg gac aac tgc cag tac gtc tac aat			2565
Gly Asp Gly Ile Leu Asn Glu Arg Asp Asn Cys Gln Tyr Val Tyr Asn			
805	810	815	
gtg gac cag aga gac act gat atg gat ggg gtt gga gat cag tgt gac			2613
Val Asp Gln Arg Asp Thr Asp Met Asp Gly Val Gly Asp Gln Cys Asp			
820	825	830	
aat tgc ccc ttg gaa cac aat ccg gat cag ctg gac tct gac tca gac			2661
Asn Cys Pro Leu Glu His Asn Pro Asp Gln Leu Asp Ser Asp Ser Asp			

835	840	845	850	
cgc att gga gat acc tgt gac aac aat cag gat att gat gaa gat ggc	2709			
Arg Ile Gly Asp Thr Cys Asp Asn Asn Gln Asp Ile Asp Glu Asp Gly				
855	860	865		
cac cag aac aat ctg gac aac tgt ccc tat gtg ccc aat gcc aac cag	2757			
His Gln Asn Asn Leu Asp Asn Cys Pro Tyr Val Pro Asn Ala Asn Gln				
870	875	880		
gct gac cat gac aaa gat ggc aag gga gat gcc tgt gac cac gat gat	2805			
Ala Asp His Asp Lys Asp Gly Lys Gly Asp Ala Cys Asp His Asp Asp				
885	890	895		
gac aac gat ggc att cct gat gac aag gac aac tgc aga ctc gtg ccc	2853			
Asp Asn Asp Gly Ile Pro Asp Asp Lys Asp Asn Cys Arg Leu Val Pro				
900	905	910		
aat ccc gac cag aag gac tct gac ggc gat ggt cga ggt gat gcc tgc	2901			
Asn Pro Asp Gln Lys Asp Ser Asp Gly Asp Gly Arg Gly Asp Ala Cys				
915	920	925	930	
aaa gat gat ttt gac cat gac agt gtg cca gac atc gat gac atc tgt	2949			
Lys Asp Asp Phe Asp His Asp Ser Val Pro Asp Ile Asp Asp Ile Cys				
935	940	945		
cct gag aat gtt gac atc agt gag acc gat ttc cgc cga ttc cag atg	2997			
Pro Glu Asn Val Asp Ile Ser Glu Thr Asp Phe Arg Arg Phe Gln Met				
950	955	960		
att cct ctg gac ccc aaa ggg aca tcc caa aat gac cct aac tgg gtt	3045			
Ile Pro Leu Asp Pro Lys Gly Thr Ser Gln Asn Asp Pro Asn Trp Val				
965	970	975		
gta cgc cat cag ggt aaa gaa ctc gtc cag act gtc aac tgt gat cct	3093			

Val Arg His Gln Gly Lys Glu Leu Val Gln Thr Val Asn Cys Asp Pro
 980 985 990
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 Gly Leu Ala Val Gly Tyr Asp Glu Phe Asn Ala Val Asp Phe Ser Gly
 995 1000 1005 1010
 acc ttc ttc atc aac acc gaa agg gac gat gac tat gct gga ttt gtc 3189
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 1015 1020 1025
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 Phe Gly Tyr Gln Ser Ser Ser Arg Phe Tyr Val Val Met Trp Lys Gln
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 Val Thr Gln Ser Tyr Trp Asp Thr Asn Pro Thr Arg Ala Gln Gly Tyr
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 Ser Gly Leu Ser Val Lys Val Val Asn Ser Thr Thr Gly Pro Gly Glu
 1060 1065 1070
 cac ctg cgg aac gcc ctg tgg cac aca gga aac acc cct ggc cag gtg 3381
 His Leu Arg Asn Ala Leu Trp His Thr Gly Asn Thr Pro Gly Gln Val
 1075 1080 1085 1090
 cgc acc ctg tgg cat gac cct cgt cac ata ggc tgg aaa gat ttc acc 3429
 Arg Thr Leu Trp His Asp Pro Arg His Ile Gly Trp Lys Asp Phe Thr
 1095 1100 1105
 gcc tac aga tgg cgt ctc agc cac agg cca aag acg ggt ttc att aga 3477
 Ala Tyr Arg Trp Arg Leu Ser His Arg Pro Lys Thr Gly Phe Ile Arg
 1110 1115 1120
 gtg gtg atg tat gaa ggg aag aaa atc atg gct gac tca gga ccc atc 3525

Val Val Met Tyr Glu Gly Lys Lys Ile Met Ala Asp Ser Gly Pro Ile

1125

1130

1135

tat gat aaa acc tat gct ggt ggt aga cta ggg ttg ttt gtc ttc tct 3573

Tyr Asp Lys Thr Tyr Ala Gly Gly Arg Leu Gly Leu Phe Val Phe Ser

1140

1145

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caa gaa atg gtg ttc ttc tct gac ctg aaa tac gaa tgt aga gat ccc 3621

Gln Glu Met Val Phe Phe Ser Asp Leu Lys Tyr Glu Cys Arg Asp Pro

1155

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1170

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5722

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<212> PRT

<213> Homo sapiens

<400> 100

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Ile Phe Glu Leu Thr Gly Ala Ala Arg Lys Gly Ser Gly Arg Arg Leu			
35	40	45	
Val Lys Gly Pro Asp Pro Ser Ser Pro Ala Phe Arg Ile Glu Asp Ala			
50	55	60	
Asn Leu Ile Pro Pro Val Pro Asp Asp Lys Phe Gln Asp Leu Val Asp			
65	70	75	80
Ala Val Arg Ala Glu Lys Gly Phe Leu Leu Leu Ala Ser Leu Arg Gln			
85	90	95	
Met Lys Lys Thr Arg Gly Thr Leu Leu Ala Leu Glu Arg Lys Asp His			
100	105	110	
Ser Gly Gln Val Phe Ser Val Val Ser Asn Gly Lys Ala Gly Thr Leu			
115	120	125	
Asp Leu Ser Leu Thr Val Gln Gly Lys Gln His Val Val Ser Val Glu			
130	135	140	
Glu Ala Leu Leu Ala Thr Gly Gln Trp Lys Ser Ile Thr Leu Phe Val			
145	150	155	160
Gln Glu Asp Arg Ala Gln Leu Tyr Ile Asp Cys Glu Lys Met Glu Asn			
165	170	175	
Ala Glu Leu Asp Val Pro Ile Gln Ser Val Phe Thr Arg Asp Leu Ala			
180	185	190	
Ser Ile Ala Arg Leu Arg Ile Ala Lys Gly Gly Val Asn Asp Asn Phe			
195	200	205	
Gln Gly Val Leu Gln Asn Val Arg Phe Val Phe Gly Thr Thr Pro Glu			
210	215	220	
Asp Ile Leu Arg Asn Lys Gly Cys Ser Ser Ser Thr Ser Val Leu Leu			
225	230	235	240

Thr Leu Asp Asn Asn Val Val Asn Gly Ser Ser Pro Ala Ile Arg Thr
245 250 255
Asn Tyr Ile Gly His Lys Thr Lys Asp Leu Gln Ala Ile Cys Gly Ile
260 265 270
Ser Cys Asp Glu Leu Ser Ser Met Val Leu Glu Leu Arg Gly Leu Arg
275 280 285
Thr Ile Val Thr Thr Leu Gln Asp Ser Ile Arg Lys Val Thr Glu Glu
290 295 300
Asn Lys Glu Leu Ala Asn Glu Leu Arg Arg Pro Pro Leu Cys Tyr His
305 310 315 320
Asn Gly Val Gln Tyr Arg Asn Asn Glu Glu Trp Thr Val Asp Ser Cys
325 330 335
Thr Glu Cys His Cys Gln Asn Ser Val Thr Ile Cys Lys Lys Val Ser
340 345 350
Cys Pro Ile Met Pro Cys Ser Asn Ala Thr Val Pro Asp Gly Glu Cys
355 360 365
Cys Pro Arg Cys Trp Pro Ser Asp Ser Ala Asp Asp Gly Trp Ser Pro
370 375 380
Trp Ser Glu Trp Thr Ser Cys Ser Thr Ser Cys Gly Asn Gly Ile Gln
385 390 395 400
Gln Arg Gly Arg Ser Cys Asp Ser Leu Asn Asn Arg Cys Glu Gly Ser
405 410 415
Ser Val Gln Thr Arg Thr Cys His Ile Gln Glu Cys Asp Lys Arg Phe
420 425 430
Lys Gln Asp Gly Gly Trp Ser His Trp Ser Pro Trp Ser Ser Cys Ser
435 440 445

Val Thr Cys Gly Asp Gly Val Ile Thr Arg Ile Arg Leu Cys Asn Ser
450 455 460
Pro Ser Pro Gln Met Asn Gly Lys Pro Cys Glu Gly Glu Ala Arg Glu
465 470 475 480
Thr Lys Ala Cys Lys Lys Asp Ala Cys Pro Ile Asn Gly Gly Trp Gly
485 490 495
Pro Trp Ser Pro Trp Asp Ile Cys Ser Val Thr Cys Gly Gly Gly Val
500 505 510
Gln Lys Arg Ser Arg Leu Cys Asn Asn Pro Ala Pro Gln Phe Gly Gly
515 520 525
Lys Asp Cys Val Gly Asp Val Thr Glu Asn Gln Ile Cys Asn Lys Gln
530 535 540
Asp Cys Pro Ile Asp Gly Cys Leu Ser Asn Pro Cys Phe Ala Gly Val
545 550 555 560
Lys Cys Thr Ser Tyr Pro Asp Gly Ser Trp Lys Cys Gly Ala Cys Pro
565 570 575
Pro Gly Tyr Ser Gly Asn Gly Ile Gln Cys Thr Asp Val Asp Glu Cys
580 585 590
Lys Glu Val Pro Asp Ala Cys Phe Asn His Asn Gly Glu His Arg Cys
595 600 605
Glu Asn Thr Asp Pro Gly Tyr Asn Cys Leu Pro Cys Pro Pro Arg Phe
610 615 620
Thr Gly Ser Gln Pro Phe Gly Gln Gly Val Glu His Ala Thr Ala Asn
625 630 635 640
Lys Gln Val Cys Lys Pro Arg Asn Pro Cys Thr Asp Gly Thr His Asp
645 650 655
Cys Asn Lys Asn Ala Lys Cys Asn Tyr Leu Gly His Tyr Ser Asp Pro

660	665	670	
Met Tyr Arg Cys Glu Cys Lys Pro Gly Tyr Ala Gly Asn Gly Ile Ile			
675	680	685	
Cys Gly Glu Asp Thr Asp Leu Asp Gly Trp Pro Asn Glu Asn Leu Val			
690	695	700	
Cys Val Ala Asn Ala Thr Tyr His Cys Lys Lys Asp Asn Cys Pro Asn			
705	710	715	720
Leu Pro Asn Ser Gly Gln Glu Asp Tyr Asp Lys Asp Gly Ile Gly Asp			
725	730	735	
Ala Cys Asp Asp Asp Asp Asp Asn Asp Lys Ile Pro Asp Asp Arg Asp			
740	745	750	
Asn Cys Pro Phe His Tyr Asn Pro Ala Gln Tyr Asp Tyr Asp Arg Asp			
755	760	765	
Asp Val Gly Asp Arg Cys Asp Asn Cys Pro Tyr Asn His Asn Pro Asp			
770	775	780	
Gln Ala Asp Thr Asp Asn Asn Gly Glu Gly Asp Ala Cys Ala Ala Asp			
785	790	795	800
Ile Asp Gly Asp Gly Ile Leu Asn Glu Arg Asp Asn Cys Gln Tyr Val			
805	810	815	
Tyr Asn Val Asp Gln Arg Asp Thr Asp Met Asp Gly Val Gly Asp Gln			
820	825	830	
Cys Asp Asn Cys Pro Leu Glu His Asn Pro Asp Gln Leu Asp Ser Asp			
835	840	845	
Ser Asp Arg Ile Gly Asp Thr Cys Asp Asn Asn Gln Asp Ile Asp Glu			
850	855	860	
Asp Gly His Gln Asn Asn Leu Asp Asn Cys Pro Tyr Val Pro Asn Ala			

865	870	875	880
Asn Gln Ala Asp His Asp Lys Asp Gly Lys Gly Asp Ala Cys Asp His			
885	890	895	
Asp Asp Asp Asn Asp Gly Ile Pro Asp Asp Lys Asp Asn Cys Arg Leu			
900	905	910	
Val Pro Asn Pro Asp Gln Lys Asp Ser Asp Gly Asp Gly Arg Gly Asp			
915	920	925	
Ala Cys Lys Asp Asp Phe Asp His Asp Ser Val Pro Asp Ile Asp Asp			
930	935	940	
Ile Cys Pro Glu Asn Val Asp Ile Ser Glu Thr Asp Phe Arg Arg Phe			
945	950	955	960
Gln Met Ile Pro Leu Asp Pro Lys Gly Thr Ser Gln Asn Asp Pro Asn			
965	970	975	
Trp Val Val Arg His Gln Gly Lys Glu Leu Val Gln Thr Val Asn Cys			
980	985	990	
Asp Pro Gly Leu Ala Val Gly Tyr Asp Glu Phe Asn Ala Val Asp Phe			
995	1000	1005	
Ser Gly Thr Phe Phe Ile Asn Thr Glu Arg Asp Asp Asp Tyr Ala Gly			
1010	1015	1020	
Phe Val Phe Gly Tyr Gln Ser Ser Ser Arg Phe Tyr Val Val Met Trp			
1025	1030	1035	1040
Lys Gln Val Thr Gln Ser Tyr Trp Asp Thr Asn Pro Thr Arg Ala Gln			
1045	1050	1055	
Gly Tyr Ser Gly Leu Ser Val Lys Val Val Asn Ser Thr Thr Gly Pro			
1060	1065	1070	
Gly Glu His Leu Arg Asn Ala Leu Trp His Thr Gly Asn Thr Pro Gly			
1075	1080	1085	

Gln Val Arg Thr Leu Trp His Asp Pro Arg His Ile Gly Trp Lys Asp

1090

1095

1100

Phe Thr Ala Tyr Arg Trp Arg Leu Ser His Arg Pro Lys Thr Gly Phe

1105

1110

1115

1120

Ile Arg Val Val Met Tyr Glu Gly Lys Lys Ile Met Ala Asp Ser Gly

1125

1130

1135

Pro Ile Tyr Asp Lys Thr Tyr Ala Gly Gly Arg Leu Gly Leu Phe Val

1140

1145

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Phe Ser Gln Glu Met Val Phe Phe Ser Asp Leu Lys Tyr Glu Cys Arg

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Asp Pro

1170

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<212> DNA

<213> Homo sapiens

<220>

<221> CDS

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<400> 101

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Met Ser Gly Gly Lys Tyr Val

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gac tcg gag gga cat ctc tac acc gtt ccc atc cgg gaa cag ggc aac 103

Asp Ser Glu Gly His Leu Tyr Thr Val Pro Ile Arg Glu Gln Gly Asn

10

15

20

atc tac aag ccc aac aac aag gcc atg gca gac gag ctg agc gag aag 151
 Ile Tyr Lys Pro Asn Asn Lys Ala Met Ala Asp Glu Leu Ser Glu Lys
 25 30 35
 caa gtg tac gac gcg cac acc aag gag atc gac ctg gtc aac cgc gac 199
 Gln Val Tyr Asp Ala His Thr Lys Glu Ile Asp Leu Val Asn Arg Asp
 40 45 50 55
 cct aaa cac ctc aac gat gac gtg gtc aag att gac ttt gaa gat gtg 247
 Pro Lys His Leu Asn Asp Asp Val Val Lys Ile Asp Phe Glu Asp Val
 60 65 70
 att gca gaa cca gaa ggg aca cac agt ttt cac ggc att tgg aag gcc 295
 Ile Ala Glu Pro Glu Gly Thr His Ser Phe His Gly Ile Trp Lys Ala
 75 80 85
 agc ttc acc acc ttc act gtg acg aaa tac tgg ttt tac cgc ttg ctg 343
 Ser Phe Thr Thr Phe Thr Val Thr Lys Tyr Trp Phe Tyr Arg Leu Leu
 90 95 100
 tct gcc ctc ttt ggc atc ccg atg gca ctc atc tgg ggc att tac ttc 391
 Ser Ala Leu Phe Gly Ile Pro Met Ala Leu Ile Trp Gly Ile Tyr Phe
 105 110 115
 gcc att ctc tct ttc ctg cac atc tgg gca gtt gta cca tgc att aag 439
 Ala Ile Leu Ser Phe Leu His Ile Trp Ala Val Val Pro Cys Ile Lys
 120 125 130 135
 agc ttc ctg att gag att cag tgc acc agc cgt gtc tat tcc atc tac 487
 Ser Phe Leu Ile Glu Ile Gln Cys Thr Ser Arg Val Tyr Ser Ile Tyr
 140 145 150
 gtc cac acc gtc tgt gac cca ctc ttt gaa gct gtt ggg aaa ata ttc 535
 Val His Thr Val Cys Asp Pro Leu Phe Glu Ala Val Gly Lys Ile Phe

155

160

165

agc aat gtc cgc atc aac ttg cag aaa gaa ata taaatgacat ttcaaggata 588

Ser Asn Val Arg Ile Asn Leu Gln Lys Glu Ile

170

175

gaagtatacc tgattttttt tccittttaat ttccclggig ccaatttcaa gtccaagtt 648

gctaatacag caacgaattt atgaattgaa ttatcttggt tgaaaataaa aagatcactt 708

tctcagtttt cataagtatt atgtctcttc tgagctatit catctatit ttggcagtcg 768

aatttttaaa acccatitatt atttctttcc ttaccttttt atttgcatgt ggalcaacca 828

tcgctttatt

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<211> 178

<212> PRT

<213> Homo sapiens

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Pro Ile Arg Glu Gln Gly Asn Ile Tyr Lys Pro Asn Asn Lys Ala Met

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30

Ala Asp Glu Leu Ser Glu Lys Gln Val Tyr Asp Ala His Thr Lys Glu

35

40

45

Ile Asp Leu Val Asn Arg Asp Pro Lys His Leu Asn Asp Asp Val Val

50

55

60

Lys Ile Asp Phe Glu Asp Val Ile Ala Glu Pro Glu Gly Thr His Ser

65

70

75

80

Phe His Gly Ile Trp Lys Ala Ser Phe Thr Thr Phe Thr Val Thr Lys

85

90

95

Tyr Trp Phe Tyr Arg Leu Leu Ser Ala Leu Phe Gly Ile Pro Met Ala

100

105

110

Leu Ile Trp Gly Ile Tyr Phe Ala Ile Leu Ser Phe Leu His Ile Trp

115

120

125

Ala Val Val Pro Cys Ile Lys Ser Phe Leu Ile Glu Ile Gln Cys Thr

130

135

140

Ser Arg Val Tyr Ser Ile Tyr Val His Thr Val Cys Asp Pro Leu Phe

145

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155

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Glu Ala Val Gly Lys Ile Phe Ser Asn Val Arg Ile Asn Leu Gln Lys

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170

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Glu Ile

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Leu Phe Leu Thr Ile Pro Phe Ala Phe Phe Leu Pro Glu Leu Ile Phe

20

25

30

ggg ttc ttg gtc tgg acc atg gta gcc gcc acc cac ata gta tac ccc 144

Gly Phe Leu Val Trp Thr Met Val Ala Ala Thr His Ile Val Tyr Pro

35

40

45

tig ctg caa gga tgg gtg atg tat gtc tcg ctc acc tcg ttt ctc atc 192

Leu Leu Gln Gly Trp Val Met Tyr Val Ser Leu Thr Ser Phe Leu Ile

50

55

60

tcc ttg atg ttc ctg ttg tct tac ttg ttt gga ttt tac aaa aga ttt 240

Ser Leu Met Phe Leu Leu Ser Tyr Leu Phe Gly Phe Tyr Lys Arg Phe

65

70

75

80

gaa tcc tgg aga gtt ctg gac agc ctg tac cac ggg acc act ggc atc 288

Glu Ser Trp Arg Val Leu Asp Ser Leu Tyr His Gly Thr Thr Gly Ile

85

90

95

ctg tac atg agc gct gcc gtc cta caa gta cat gcc acg att gtt tct 336

Leu Tyr Met Ser Ala Ala Val Leu Gln Val His Ala Thr Ile Val Ser

100

105

110

gag aaa ctg ctg gac cca aga att tac tac att aat tcg gca gcc tcg 384

Glu Lys Leu Leu Asp Pro Arg Ile Tyr Tyr Ile Asn Ser Ala Ala Ser

115

120

125

ttc ttc gcc ttc atc gcc acg ctg ctc tac att ctc cat gcc ttc agc 432

Phe Phe Ala Phe Ile Ala Thr Leu Leu Tyr Ile Leu His Ala Phe Ser

130

135

140

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Ile Tyr Tyr His

145

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gaagateccac taaaacgtcc acgggattaa cagaacgtcc ttgcagactg agcgatgaca 604

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 tctttttttt gtttgtttta ttltgttttt ttltgagacgg agtcctgctc ttctccaag 904
 gctggagtgc agtgacgca tctccactca ctgcaggctc cgcctcccg gttcccgcca 964
 ttctctgcc tcagcctccc gagtagccgg gactacaggc gccaccacc atgcccggct 1024
 aatttagttg tttttttagt agagatgggg ttccaccgta ttagccagga tggctctgat 1084
 ctctgacct cgtgatccgc cgcctcggc ctcccaaagt gctgggatta caggcgtgag 1144
 ccaccgtgcc cggcctgatt ctcttaaaat tgaagaggtg ctgccaagc ctccagatct 1204
 aacgcagatg catagacctt gtctctggta ctgttcagc ctgtgctggg gagccgtggt 1264
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 cctcccttt cctctccagc attaggattc aagggaatc tgcattgaag caattttgag 1384
 ggtagacgtg tggggaaaat aaatcattat acagtaagac ctggggcttg aggggtggg 1444
 aatggggagg gaaggcata gccgtctct ccatgagct gacatctcg aaactgagca 1504
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 ctaaagaaag ctgtgtctt ctgtgacc agacgaatag ggcacagccc tgtaactgca 1924
 cgtgccctct gtcattgga atgaaataa ttattacgag aaaggactt gtcctaactg 1984
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<210> 104

<211> 148

<212> PRT

<213> Homo sapiens

<400> 104

Pro Pro Ala Thr Ser Tyr Ala Pro Ser Asp Val Pro Ser Gly Val Ala

1 5 10 15

Leu Phe Leu Thr Ile Pro Phe Ala Phe Phe Leu Pro Glu Leu Ile Phe

20 25 30

Gly Phe Leu Val Trp Thr Met Val Ala Ala Thr His Ile Val Tyr Pro

35 40 45

Leu Leu Gln Gly Trp Val Met Tyr Val Ser Leu Thr Ser Phe Leu Ile

50 55 60

Ser Leu Met Phe Leu Leu Ser Tyr Leu Phe Gly Phe Tyr Lys Arg Phe

65 70 75 80

Glu Ser Trp Arg Val Leu Asp Ser Leu Tyr His Gly Thr Thr Gly Ile

85 90 95

Leu Tyr Met Ser Ala Ala Val Leu Gln Val His Ala Thr Ile Val Ser

100 105 110

Glu Lys Leu Leu Asp Pro Arg Ile Tyr Tyr Ile Asn Ser Ala Ala Ser

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Phe Phe Ala Phe Ile Ala Thr Leu Leu Tyr Ile Leu His Ala Phe Ser

130 135 140

Ile Tyr Tyr His

145

<210> 105

<211> 2899

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (91).. (2196)

<400> 105

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 gggcctcggc tacttggact gcggcggaat atg gcg gct ccg atg act ccc gcg 114

Met Ala Ala Pro Met Thr Pro Ala

1

5

gct cgg ccc gag gac tac gag gcg gcg ctc aat gcc gcc ctg gct gac 162

Ala Arg Pro Glu Asp Tyr Glu Ala Ala Leu Asn Ala Ala Leu Ala Asp

10

15

20

gtg ccc gaa ctg gcc aga ctc ctg gag atc gac ccg tac ttg aag ccc 210

Val Pro Glu Leu Ala Arg Leu Leu Glu Ile Asp Pro Tyr Leu Lys Pro

25

30

35

40

tac gcc gtg gac ttc cag cgc agg tat aag cag ttt agc caa att ttg 258

Tyr Ala Val Asp Phe Gln Arg Arg Tyr Lys Gln Phe Ser Gln Ile Leu

45

50

55

aag aac att gga gaa aat gaa ggt ggt att gat aag ttt tcc aga ggc 306

Lys Asn Ile Gly Glu Asn Glu Gly Gly Ile Asp Lys Phe Ser Arg Gly

60

65

70

tat gaa tca ttt ggc gtc cac aga tgt gct gat ggt ggt tta tac tcc 354

Tyr Glu Ser Phe Gly Val His Arg Cys Ala Asp Gly Gly Leu Tyr Ser

75

80

85

aaa gaa tgg gcc ccg gga gca gaa gga gtt ttt ctt act gga gat ttt 402
 Lys Glu Trp Ala Pro Gly Ala Glu Gly Val Phe Leu Thr Gly Asp Phe
 90 95 100
 aat ggt tgg aat cca ttt tgg tac cca tac aaa aaa ctg gat tat gga 450
 Asn Gly Trp Asn Pro Phe Ser Tyr Pro Tyr Lys Lys Leu Asp Tyr Gly
 105 110 115 120
 aaa tgg gag ctg tat atc cca cca aag cag aat aaa tct gta ctc gtg 498
 Lys Trp Glu Leu Tyr Ile Pro Pro Lys Gln Asn Lys Ser Val Leu Val
 125 130 135
 cct cat gga tcc aaa tta aag gta gtt att act agt aaa agc gga gag 546
 Pro His Gly Ser Lys Leu Lys Val Val Ile Thr Ser Lys Ser Gly Glu
 140 145 150
 atc ttg tat cgt att tca ccg tgg gca aag tat gtg gtt cgt gaa ggt 594
 Ile Leu Tyr Arg Ile Ser Pro Trp Ala Lys Tyr Val Val Arg Glu Gly
 155 160 165
 gat aat gtg aat tat gat tgg ata cac tgg gat cca gaa cac tca tat 642
 Asp Asn Val Asn Tyr Asp Trp Ile His Trp Asp Pro Glu His Ser Tyr
 170 175 180
 gag ttt aag cat tcc aga cca aag aag cca cgg agt cta aga att tat 690
 Glu Phe Lys His Ser Arg Pro Lys Lys Pro Arg Ser Leu Arg Ile Tyr
 185 190 195 200
 gaa tct cat gtg gga att tct tcc cat gaa gga aaa gta gct tct tat 738
 Glu Ser His Val Gly Ile Ser Ser His Glu Gly Lys Val Ala Ser Tyr
 205 210 215
 aaa cat ttt aca tgc aat gta cta cca aga atc aaa ggc ctt gga tac 786
 Lys His Phe Thr Cys Asn Val Leu Pro Arg Ile Lys Gly Leu Gly Tyr
 220 225 230

aac tgc att cag ttg atg gca atc atg gag cat gct tac tat gcc agc 834
 Asn Cys Ile Gln Leu Met Ala Ile Met Glu His Ala Tyr Tyr Ala Ser
 235 240 245
 ttt ggt tac caa atc aca agc ttc ttt gca gct tcc agc cgt tat gga 882
 Phe Gly Tyr Gln Ile Thr Ser Phe Phe Ala Ala Ser Ser Arg Tyr Gly
 250 255 260
 aca cct gaa gag cta caa gaa ctg gta gac aca gct cat tcc atg ggt 930
 Thr Pro Glu Glu Leu Gln Glu Leu Val Asp Thr Ala His Ser Met Gly
 265 270 275 280
 atc ata gtc ctc tta gat gtg gta cac agc cat gct tca aaa aat tca 978
 Ile Ile Val Leu Leu Asp Val Val His Ser His Ala Ser Lys Asn Ser
 285 290 295
 gca gat gga ttg aat atg ttt gat ggg aca gat tcc tgt tat ttt cat 1026
 Ala Asp Gly Leu Asn Met Phe Asp Gly Thr Asp Ser Cys Tyr Phe His
 300 305 310
 tct gga cct aga ggg act cat gat ctt tgg gat agc aga ttg ttt gcc 1074
 Ser Gly Pro Arg Gly Thr His Asp Leu Trp Asp Ser Arg Leu Phe Ala
 315 320 325
 tac tcc agc tgg gaa gtt tta aga ttc ctt ctg tca aac ata aga tgg 1122
 Tyr Ser Ser Trp Glu Val Leu Arg Phe Leu Leu Ser Asn Ile Arg Trp
 330 335 340
 tgg ttg gaa gaa tat cgc ttt gat gga ttt cgt ttt gat ggt gtt acg 1170
 Trp Leu Glu Glu Tyr Arg Phe Asp Gly Phe Arg Phe Asp Gly Val Thr
 345 350 355 360
 tcc atg ctt tat cat cac cat gga glg ggt caa ggt ttc tca ggt gat 1218
 Ser Met Leu Tyr His His His Gly Val Gly Gln Gly Phe Ser Gly Asp

365	370	375	
tac agt gaa tat ttc gga cta caa gta gat gaa gat gcc ttg act tac			1266
Tyr Ser Glu Tyr Phe Gly Leu Gln Val Asp Glu Asp Ala Leu Thr Tyr			
380	385	390	
ctc atg ttg gca aat cat ttg gti cac acg ctg tgt ccc gat tct ata			1314
Leu Met Leu Ala Asn His Leu Val His Thr Leu Cys Pro Asp Ser Ile			
395	400	405	
aca ata gct gag gat gta tca gga atg cca gct ctg tgc tct cca att			1362
Thr Ile Ala Glu Asp Val Ser Gly Met Pro Ala Leu Cys Ser Pro Ile			
410	415	420	
tcc cag gga ggg ggt ggt ttt gac tat cga cta gcc atg gca att cca			1410
Ser Gln Gly Gly Gly Gly Phe Asp Tyr Arg Leu Ala Met Ala Ile Pro			
425	430	435	440
gat aag tgg att cag cta ctt aaa gag ttt aaa gat gaa gac tgg aac			1458
Asp Lys Trp Ile Gln Leu Leu Lys Glu Phe Lys Asp Glu Asp Trp Asn			
445	450	455	
atg ggc gat ata gta tac acg ctc aca aac agg cgc tac ctt gaa aag			1506
Met Gly Asp Ile Val Tyr Thr Leu Thr Asn Arg Arg Tyr Leu Glu Lys			
460	465	470	
tgc att gct tat gca gag agc cat gat cag gca ttg gti ggg gat aag			1554
Cys Ile Ala Tyr Ala Glu Ser His Asp Gln Ala Leu Val Gly Asp Lys			
475	480	485	
tgc ctg gca ttt tgg ttg atg gat gcc gaa atg tat aca aac atg agt			1602
Ser Leu Ala Phe Trp Leu Met Asp Ala Glu Met Tyr Thr Asn Met Ser			
490	495	500	
gtc ctg act cct ttt act cca gtt att gat cgt gga ata cag ctt cat			1650
Val Leu Thr Pro Phe Thr Pro Val Ile Asp Arg Gly Ile Gln Leu His			

505	510	515	520	
aaa atg att cga ctc att acg cat ggg ctt ggt gga gaa ggc tat ctc	1698			
Lys Met Ile Arg Leu Ile Thr His Gly Leu Gly Gly Glu Gly Tyr Leu				
525	530	535		
aat ttc atg ggt aat gaa ttt ggg cat cct gaa tgg tta gac ttc cca	1746			
Asn Phe Met Gly Asn Glu Phe Gly His Pro Glu Trp Leu Asp Phe Pro				
540	545	550		
aga aaa gga aat aat gag agt tac cat tat gcc agg cgg cag ttt cat	1794			
Arg Lys Gly Asn Asn Glu Ser Tyr His Tyr Ala Arg Arg Gln Phe His				
555	560	565		
tta act gac gac gac ctt ctt cgc tac aag ttc cta aat aat ttt gac	1842			
Leu Thr Asp Asp Asp Leu Leu Arg Tyr Lys Phe Leu Asn Asn Phe Asp				
570	575	580		
agg gat atg aat aga ttg gaa gaa aga tat ggt tgg ctt gca gct cca	1890			
Arg Asp Met Asn Arg Leu Glu Glu Arg Tyr Gly Trp Leu Ala Ala Pro				
585	590	595	600	
cag gcc tac glg agt gaa aaa cat gaa ggc aat aag atc att gct ttt	1938			
Gln Ala Tyr Val Ser Glu Lys His Glu Gly Asn Lys Ile Ile Ala Phe				
605	610	615		
gaa aga gca ggt ctt ctt ttc att ttc aac ttc cat cca agc aag agc	1986			
Glu Arg Ala Gly Leu Leu Phe Ile Phe Asn Phe His Pro Ser Lys Ser				
620	625	630		
tac act gac tac cga gtt gga aca gca ttg cca ggg aaa ttc aaa att	2034			
Tyr Thr Asp Tyr Arg Val Gly Thr Ala Leu Pro Gly Lys Phe Lys Ile				
635	640	645		
gtg cta gat tca gat gca gcg gaa tat gga ggg cat cag aga ctg gac	2082			

Val Leu Asp Ser Asp Ala Ala Glu Tyr Gly Gly His Gln Arg Leu Asp

650

655

660

cac agc act gac ttt ttt tct gag gct ttt gaa cat aat ggg cgt ccc 2130

His Ser Thr Asp Phe Phe Ser Glu Ala Phe Glu His Asn Gly Arg Pro

665

670

675

680

tat tct ctt ttg gtg tac att cca agc aga gtg gcc ctc atc ctt cag 2178

Tyr Ser Leu Leu Val Tyr Ile Pro Ser Arg Val Ala Leu Ile Leu Gln

685

690

695

aat gtg gat ctg ccg aat tgaagaggcc tgatttcagc tccaccagat 2226

Asn Val Asp Leu Pro Asn

700

gcagatttgt gtittgtttt ctgtttatca ctgtcacaca gcattataca tgtatgcitt 2286

tcagaalaca gttgtctagc caagccatca agtgtctgaa attcaatatt ggtttatgca 2346

aatacagcaa acttttattt aagtagatag gagaatatgt ttaaaatatt aggaatccta 2406

gaccataatt tcaagtcac tttagcagcta ggattctcaa atggaagtgt tatatataat 2466

atgttaaaaa cattttgctt tcttggctaa ttatttgatc cttttaaatc caaatttgaa 2526

tcatttgica tgtatgatta ttctgttaa atgtacacag tatttaagat ggatatttgg 2586

tggcctciatt tgttctgata tcttttggc taaattatga ggtaccaaga ttgtttcttt 2646

gtttcttttt ttcaaattgt gtttagaaat actgtaataa atatgcagta gtgatataaa 2706

gaattataic caaggtaata taaaagccat tacgtatgaa ctcatccgtg tctcattttg 2766

tgttttattt tgtatctct tgtccactaa gtatcttggt aaatgccagt atctcagict 2826

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aaaaagcttt tgi 2899

<210> 106

<211> 702

<212> PRT

<213> Homo sapiens

<400> 106

Met Ala Ala Pro Met Thr Pro Ala Ala Arg Pro Glu Asp Tyr Glu Ala

1 5 10 15

Ala Leu Asn Ala Ala Leu Ala Asp Val Pro Glu Leu Ala Arg Leu Leu

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Glu Ile Asp Pro Tyr Leu Lys Pro Tyr Ala Val Asp Phe Gln Arg Arg

35 40 45

Tyr Lys Gln Phe Ser Gln Ile Leu Lys Asn Ile Gly Glu Asn Glu Gly

50 55 60

Gly Ile Asp Lys Phe Ser Arg Gly Tyr Glu Ser Phe Gly Val His Arg

65 70 75 80

Cys Ala Asp Gly Gly Leu Tyr Ser Lys Glu Trp Ala Pro Gly Ala Glu

85 90 95

Gly Val Phe Leu Thr Gly Asp Phe Asn Gly Trp Asn Pro Phe Ser Tyr

100 105 110

Pro Tyr Lys Lys Leu Asp Tyr Gly Lys Trp Glu Leu Tyr Ile Pro Pro

115 120 125

Lys Gln Asn Lys Ser Val Leu Val Pro His Gly Ser Lys Leu Lys Val

130 135 140

Val Ile Thr Ser Lys Ser Gly Glu Ile Leu Tyr Arg Ile Ser Pro Trp

145 150 155 160

Ala Lys Tyr Val Val Arg Glu Gly Asp Asn Val Asn Tyr Asp Trp Ile

165 170 175

His Trp Asp Pro Glu His Ser Tyr Glu Phe Lys His Ser Arg Pro Lys

180 185 190

Lys Pro Arg Ser Leu Arg Ile Tyr Glu Ser His Val Gly Ile Ser Ser

195	200	205	
His Glu Gly Lys Val Ala Ser Tyr Lys His Phe Thr Cys Asn Val Leu			
210	215	220	
Pro Arg Ile Lys Gly Leu Gly Tyr Asn Cys Ile Gln Leu Met Ala Ile			
225	230	235	240
Met Glu His Ala Tyr Tyr Ala Ser Phe Gly Tyr Gln Ile Thr Ser Phe			
	245	250	255
Phe Ala Ala Ser Ser Arg Tyr Gly Thr Pro Glu Glu Leu Gln Glu Leu			
	260	265	270
Val Asp Thr Ala His Ser Met Gly Ile Ile Val Leu Leu Asp Val Val			
275	280	285	
His Ser His Ala Ser Lys Asn Ser Ala Asp Gly Leu Asn Met Phe Asp			
290	295	300	
Gly Thr Asp Ser Cys Tyr Phe His Ser Gly Pro Arg Gly Thr His Asp			
305	310	315	320
Leu Trp Asp Ser Arg Leu Phe Ala Tyr Ser Ser Trp Glu Val Leu Arg			
	325	330	335
Phe Leu Leu Ser Asn Ile Arg Trp Trp Leu Glu Glu Tyr Arg Phe Asp			
	340	345	350
Gly Phe Arg Phe Asp Gly Val Thr Ser Met Leu Tyr His His His Gly			
355	360	365	
Val Gly Gln Gly Phe Ser Gly Asp Tyr Ser Glu Tyr Phe Gly Leu Gln			
370	375	380	
Val Asp Glu Asp Ala Leu Thr Tyr Leu Met Leu Ala Asn His Leu Val			
385	390	395	400
His Thr Leu Cys Pro Asp Ser Ile Thr Ile Ala Glu Asp Val Ser Gly			

405	410	415	
Met Pro Ala Leu Cys Ser Pro Ile Ser Gln Gly Gly Gly Phe Asp			
420	425	430	
Tyr Arg Leu Ala Met Ala Ile Pro Asp Lys Trp Ile Gln Leu Leu Lys			
435	440	445	
Glu Phe Lys Asp Glu Asp Trp Asn Met Gly Asp Ile Val Tyr Thr Leu			
450	455	460	
Thr Asn Arg Arg Tyr Leu Glu Lys Cys Ile Ala Tyr Ala Glu Ser His			
465	470	475	480
Asp Gln Ala Leu Val Gly Asp Lys Ser Leu Ala Phe Trp Leu Met Asp			
485	490	495	
Ala Glu Met Tyr Thr Asn Met Ser Val Leu Thr Pro Phe Thr Pro Val			
500	505	510	
Ile Asp Arg Gly Ile Gln Leu His Lys Met Ile Arg Leu Ile Thr His			
515	520	525	
Gly Leu Gly Gly Glu Gly Tyr Leu Asn Phe Met Gly Asn Glu Phe Gly			
530	535	540	
His Pro Glu Trp Leu Asp Phe Pro Arg Lys Gly Asn Asn Glu Ser Tyr			
545	550	555	560
His Tyr Ala Arg Arg Gln Phe His Leu Thr Asp Asp Asp Leu Leu Arg			
565	570	575	
Tyr Lys Phe Leu Asn Asn Phe Asp Arg Asp Met Asn Arg Leu Glu Glu			
580	585	590	
Arg Tyr Gly Trp Leu Ala Ala Pro Gln Ala Tyr Val Ser Glu Lys His			
595	600	605	
Glu Gly Asn Lys Ile Ile Ala Phe Glu Arg Ala Gly Leu Leu Phe Ile			
610	615	620	

Phe Asn Phe His Pro Ser Lys Ser Tyr Thr Asp Tyr Arg Val Gly Thr

625 630 635 640

Ala Leu Pro Gly Lys Phe Lys Ile Val Leu Asp Ser Asp Ala Ala Glu

645 650 655

Tyr Gly Gly His Gln Arg Leu Asp His Ser Thr Asp Phe Phe Ser Glu

660 665 670

Ala Phe Glu His Asn Gly Arg Pro Tyr Ser Leu Leu Val Tyr Ile Pro

675 680 685

Ser Arg Val Ala Leu Ile Leu Gln Asn Val Asp Leu Pro Asn

690 695 700

<210> 107

<211> 790

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (78).. (626)

<400> 107

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tctccttagt cgccgcc atg acg acc gcg tcc acc tcg cag gtg cgc cag 110

Met Thr Thr Ala Ser Thr Ser Gln Val Arg Gln

1 5 10

aac tac cac cag gac tca gag gcc gcc atc aac cgc cag atc aac ctg 158

Asn Tyr His Gln Asp Ser Glu Ala Ala Ile Asn Arg Gln Ile Asn Leu

15 20 25

gag ctc tac gcc tcc tac gtt tac ctg tcc atg tct tac tac ttt gac 206

Glu Leu Tyr Ala Ser Tyr Val Tyr Leu Ser Met Ser Tyr Tyr Phe Asp
 30 35 40
 cgc gat gat gtg gct ttg aag aac ttt gcc aaa tac ttt ctt cac caa 254
 Arg Asp Asp Val Ala Leu Lys Asn Phe Ala Lys Tyr Phe Leu His Gln
 45 50 55
 tct cat gag gag agg gaa cat gct gag aaa ctg atg aag ctg cag aac 302
 Ser His Glu Glu Arg Glu His Ala Glu Lys Leu Met Lys Leu Gln Asn
 60 65 70 75
 caa cga ggt ggc cga atc ttc ctt cag gat atc aag aaa cca gac tgt 350
 Gln Arg Gly Gly Arg Ile Phe Leu Gln Asp Ile Lys Lys Pro Asp Cys
 80 85 90
 gat gac tgg gag agc ggg ctg aat gca atg gag tgt gca tta cat ttg 398
 Asp Asp Trp Glu Ser Gly Leu Asn Ala Met Glu Cys Ala Leu His Leu
 95 100 105
 gaa aaa aat gtg aat cag tca cta ctg gaa ctg cac aaa ctg gcc act 446
 Glu Lys Asn Val Asn Gln Ser Leu Leu Glu Leu His Lys Leu Ala Thr
 110 115 120
 gac aaa aat gac ccc cat ttg tgt gac ttc att gag aca cat tac ctg 494
 Asp Lys Asn Asp Pro His Leu Cys Asp Phe Ile Glu Thr His Tyr Leu
 125 130 135
 aat gag cag gtg aaa gcc atc aaa gaa ttg ggt gac cac gtg acc aac 542
 Asn Glu Gln Val Lys Ala Ile Lys Glu Leu Gly Asp His Val Thr Asn
 140 145 150 155
 ttg cgc aag atg gga gcg ccc gaa tct ggc ttg gcg gaa tat ctc ttt 590
 Leu Arg Lys Met Gly Ala Pro Glu Ser Gly Leu Ala Glu Tyr Leu Phe
 160 165 170

gac aag cac acc ctg gga gac agt gat aat gaa agc taagccctgg 636

Asp Lys His Thr Leu Gly Asp Ser Asp Asn Glu Ser

175

180

gctaatttcc ccatagccgt ggggtgacct ccttggtcac caaggcagtg catgcatgtt 696

ggggtttccct ttaccttttc tataagltgt accaaaacat ccacttaagt tctttgattt 756

gtaccattcc ttcaaataaa gaaatttggg accc 790

<210> 108

<211> 183

<212> PRT

<213> Homo sapiens

<400> 108

Met Thr Thr Ala Ser Thr Ser Gln Val Arg Gln Asn Tyr His Gln Asp

1

5

10

15

Ser Glu Ala Ala Ile Asn Arg Gln Ile Asn Leu Glu Leu Tyr Ala Ser

20

25

30

Tyr Val Tyr Leu Ser Met Ser Tyr Tyr Phe Asp Arg Asp Asp Val Ala

35

40

45

Leu Lys Asn Phe Ala Lys Tyr Phe Leu His Gln Ser His Glu Glu Arg

50

55

60

Glu His Ala Glu Lys Leu Met Lys Leu Gln Asn Gln Arg Gly Gly Arg

65

70

75

80

Ile Phe Leu Gln Asp Ile Lys Lys Pro Asp Cys Asp Asp Trp Glu Ser

85

90

95

Gly Leu Asn Ala Met Glu Cys Ala Leu His Leu Glu Lys Asn Val Asn

100

105

110

Gln Ser Leu Leu Glu Leu His Lys Leu Ala Thr Asp Lys Asn Asp Pro

115 120 125
 His Leu Cys Asp Phe Ile Glu Thr His Tyr Leu Asn Glu Gln Val Lys
 130 135 140
 Ala Ile Lys Glu Leu Gly Asp His Val Thr Asn Leu Arg Lys Met Gly
 145 150 155 160
 Ala Pro Glu Ser Gly Leu Ala Glu Tyr Leu Phe Asp Lys His Thr Leu
 165 170 175
 Gly Asp Ser Asp Asn Glu Ser
 180

<210> 109

<211> 3460

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (256).. (1857)

<400> 109

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 gggctgggct gtgcgccigc gcagtgtggg tcgtcccga ttccctgccc cggccggccc 180
 cgctcggct ccgcacccctc gcccgcctct cagccgccgc tctgccccgc agcagccagc 240
 cccgtgtccg gcagt atg ttc agc tgg gtc agc aag gat gcc cgc cgc aag 291

Met Phe Ser Trp Val Ser Lys Asp Ala Arg Arg Lys

1

5

10

aag gag ccg gag ctc ttc cag acg gtg gcc gag ggg ctg cgg cag ctg 339

Lys Glu Pro Glu Leu Phe Gln Thr Val Ala Glu Gly Leu Arg Gln Leu

15	20	25	
tac gcg cag aag ctg cta ccc ctg gag gag cac tac cgc ttc cac gag	387		
Tyr Ala Gln Lys Leu Leu Pro Leu Glu Glu His Tyr Arg Phe His Glu			
30	35	40	
ttc cac tgc ccc gcr ctg gag gac gct gac ttc gac aac aag cct atg	435		
Phe His Ser Pro Xaa Leu Glu Asp Ala Asp Phe Asp Asn Lys Pro Met			
45	50	55	60
gtg ctc ctc gtg rgg cag tac agc acg ggc aag acc acc ttc atc cga	483		
Val Leu Leu Val Xaa Gln Tyr Ser Thr Gly Lys Thr Thr Phe Ile Arg			
65	70	75	
cac ctg atc gag cag gac ttc ccg ggg atg cgc atc ggg ccc gag ccc	531		
His Leu Ile Glu Gln Asp Phe Pro Gly Met Arg Ile Gly Pro Glu Pro			
80	85	90	
acc acc gac tcc ttc atc gcc gtc atg cac ggc ccc act gag ggc gtg	579		
Thr Thr Asp Ser Phe Ile Ala Val Met His Gly Pro Thr Glu Gly Val			
95	100	105	
gtg ccg ggc aac gcg ctc gtg gtg gac ccg cgg cgc ccc ttc cgc aag	627		
Val Pro Gly Asn Ala Leu Val Val Asp Pro Arg Arg Pro Phe Arg Lys			
110	115	120	
ctc aac gcg ttt ggc aac gct ttc ctc aac agg ttc atg tgt gcc cag	675		
Leu Asn Ala Phe Gly Asn Ala Phe Leu Asn Arg Phe Met Cys Ala Gln			
125	130	135	140
ctg ccc aac ccc gtc ctg gac agc atc agc atc atc gac acc ccc ggg	723		
Leu Pro Asn Pro Val Leu Asp Ser Ile Ser Ile Ile Asp Thr Pro Gly			
145	150	155	
atc ctg tct gga gag aag cag cgg atc agc aga ggc tat gac ttt gca	771		
Ile Leu Ser Gly Glu Lys Gln Arg Ile Ser Arg Gly Tyr Asp Phe Ala			

160	165	170	
gcc gtc ctg gag tgg ttc gcg gag cgt gtg gac cgc atc atc ctg ctc	819		
Ala Val Leu Glu Trp Phe Ala Glu Arg Val Asp Arg Ile Ile Leu Leu			
175	180	185	
ttc gac gcc cac aag ctg gac atc tcc gat gag ttc tcg gaa gtg atc	867		
Phe Asp Ala His Lys Leu Asp Ile Ser Asp Glu Phe Ser Glu Val Ile			
190	195	200	
aag gct ctg aag aac cat gag gac aag atc cgc gtg gtg ctg aac aag	915		
Lys Ala Leu Lys Asn His Glu Asp Lys Ile Arg Val Val Leu Asn Lys			
205	210	215	220
gca gac cag atc gag acg cag cag ctg atg cgg gtg tac ggg gcc ctc	963		
Ala Asp Gln Ile Glu Thr Gln Gln Leu Met Arg Val Tyr Gly Ala Leu			
225	230	235	
atg tgg tcc ctg ggc aag atc atc aac acc ccc gag gtg gtc agg gtc	1011		
Met Trp Ser Leu Gly Lys Ile Ile Asn Thr Pro Glu Val Val Arg Val			
240	245	250	
tac atc ggc tcc ttc tgg tcc cac ccg ctc ctc atc ccc gac aac cgc	1059		
Tyr Ile Gly Ser Phe Trp Ser His Pro Leu Leu Ile Pro Asp Asn Arg			
255	260	265	
aag ctc ttt gag gcc gag gag cag gac ctc ttc aag gac atc cag tca	1107		
Lys Leu Phe Glu Ala Glu Glu Gln Asp Leu Phe Lys Asp Ile Gln Ser			
270	275	280	
ctg ccc cga aac gcc gcc ctc agg aag ctc aat gac ctg atc aag cgg	1155		
Leu Pro Arg Asn Ala Ala Leu Arg Lys Leu Asn Asp Leu Ile Lys Arg			
285	290	295	300
gca cgg ctg gcc aag gtt cac gcc tac atc atc agc tcc ctc aag aaa	1203		

Ala Arg Leu Ala Lys Val His Ala Tyr Ile Ile Ser Ser Leu Lys Lys

305

310

315

gag atg ccc aat gtc ttt ggt aaa gag agc aaa aag aaa gag ctg gtg 1251

Glu Met Pro Asn Val Phe Gly^oLys Glu Ser Lys Lys Lys Glu Leu Val

320

325

330

aac aac ctg gga gag atc tac cag aag att gag cgc gag cac cag atc 1299

Asn Asn Leu Gly Glu Ile Tyr Gln Lys Ile Glu Arg Glu His Gln Ile

335

340

345

tcc cct ggg gac ttc ccg agc ctc cgc aag atg cag gaa ctc ctg cag 1347

Ser Pro Gly Asp Phe Pro Ser Leu Arg Lys Met Gln Glu Leu Leu Gln

350

355

360

acc cag gac ttc agc aag ttc cag gcg ctg aag ccc aag ctg ctg gac 1395

Thr Gln Asp Phe Ser Lys Phe Gln Ala Leu Lys Pro Lys Leu Leu Asp

365

370

375

380

acg gtg gat gac atg ctg gcc aac gac atc gcg cgg ctg atg gtg atg 1443

Thr Val Asp Asp Met Leu Ala Asn Asp Ile Ala Arg Leu Met Val Met

385

390

395

gtg cgg cag gag gag tcc ctg atg cct tcc cag gtg gtc aag ggc ggc 1491

Val Arg Gln Glu Glu Ser Leu Met Pro Ser Gln Val Val Lys Gly Gly

400

405

410

gcc ttt gac ggc acc atg aac ggg ccg ttc ggg cac ggc tac ggc gag 1539

Ala Phe Asp Gly Thr Met Asn Gly Pro Phe Gly His Gly Tyr Gly Glu

415

420

425

ggg gcc ggc gag ggc atc cac gac gtg gag tgg gtg gtg ggc aag gac 1587

Gly Ala Gly Glu Gly Ile His Asp Val Glu Trp Val Val Gly Lys Asp

430

435

440

aag ccc acc tac gac gag atc ttc tac acg ctg tcc cct gtc aac ggc 1635

Lys Pro Thr Tyr Asp Glu Ile Phe Tyr Thr Leu Ser Pro Val Asn Gly
 445 450 455 460
 aag atc acg ggc gcc aac gcc aag aag gag atg gtg aag tcc aag ctc 1683
 Lys Ile Thr Gly Ala Asn Ala Lys Lys Glu Met Val Lys Ser Lys Leu
 465 470 475
 ccc aac acc gtg cta ggg aag atc tgg aag ctg gcc gac gtg gac aag 1731
 Pro Asn Thr Val Leu Gly Lys Ile Trp Lys Leu Ala Asp Val Asp Lys
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 gac ggg ctg ctg gac gac gag gag ttc gcg ctg gcc aac cac ctc atc 1779
 Asp Gly Leu Leu Asp Asp Glu Glu Phe Ala Leu Ala Asn His Leu Ile
 495 500 505
 aag gtc aag ctg gag ggc cac gag ctg ccc gcc gac ctg ccc ccg cac 1827
 Lys Val Lys Leu Glu Gly His Glu Leu Pro Ala Asp Leu Pro Pro His
 510 515 520
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 Leu Val Pro Pro Ser Lys Arg Arg His Glu
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<211> 534

<212> PRT

<213> Homo sapiens

<400> 110

Met Phe Ser Trp Val Ser Lys Asp Ala Arg Arg Lys Lys Glu Pro Glu

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10

15

Leu Phe Gln Thr Val Ala Glu Gly Leu Arg Gln Leu Tyr Ala Gln Lys

20	25	30	
Leu Leu Pro Leu Glu Glu His Tyr Arg Phe His Glu Phe His Ser Pro			
35	40	45	
Xaa Leu Glu Asp Ala Asp Phe Asp Asn Lys Pro Met Val Leu Leu Val			
50	55	60	
Xaa Gln Tyr Ser Thr Gly Lys Thr Thr Phe Ile Arg His Leu Ile Glu			
65	70	75	80
Gln Asp Phe Pro Gly Met Arg Ile Gly Pro Glu Pro Thr Thr Asp Ser			
85	90	95	
Phe Ile Ala Val Met His Gly Pro Thr Glu Gly Val Val Pro Gly Asn			
100	105	110	
Ala Leu Val Val Asp Pro Arg Arg Pro Phe Arg Lys Leu Asn Ala Phe			
115	120	125	
Gly Asn Ala Phe Leu Asn Arg Phe Met Cys Ala Gln Leu Pro Asn Pro			
130	135	140	
Val Leu Asp Ser Ile Ser Ile Ile Asp Thr Pro Gly Ile Leu Ser Gly			
145	150	155	160
Glu Lys Gln Arg Ile Ser Arg Gly Tyr Asp Phe Ala Ala Val Leu Glu			
165	170	175	
Trp Phe Ala Glu Arg Val Asp Arg Ile Ile Leu Leu Phe Asp Ala His			
180	185	190	
Lys Leu Asp Ile Ser Asp Glu Phe Ser Glu Val Ile Lys Ala Leu Lys			
195	200	205	
Asn His Glu Asp Lys Ile Arg Val Val Leu Asn Lys Ala Asp Gln Ile			
210	215	220	
Glu Thr Gln Gln Leu Met Arg Val Tyr Gly Ala Leu Met Trp Ser Leu			
225	230	235	240

Gly Lys Ile Ile Asn Thr Pro Glu Val Val Arg Val Tyr Ile Gly Ser

245

250

255

Phe Trp Ser His Pro Leu Leu Ile Pro Asp Asn Arg Lys Leu Phe Glu

260

265

270

Ala Glu Glu Gln Asp Leu Phe Lys Asp Ile Gln Ser Leu Pro Arg Asn

275

280

285

Ala Ala Leu Arg Lys Leu Asn Asp Leu Ile Lys Arg Ala Arg Leu Ala

290

295

300

Lys Val His Ala Tyr Ile Ile Ser Ser Leu Lys Lys Glu Met Pro Asn

305

310

315

320

Val Phe Gly Lys Glu Ser Lys Lys Lys Glu Leu Val Asn Asn Leu Gly

325

330

335

Glu Ile Tyr Gln Lys Ile Glu Arg Glu His Gln Ile Ser Pro Gly Asp

340

345

350

Phe Pro Ser Leu Arg Lys Met Gln Glu Leu Leu Gln Thr Gln Asp Phe

355

360

365

Ser Lys Phe Gln Ala Leu Lys Pro Lys Leu Leu Asp Thr Val Asp Asp

370

375

380

Met Leu Ala Asn Asp Ile Ala Arg Leu Met Val Met Val Arg Gln Glu

385

390

395

400

Glu Ser Leu Met Pro Ser Gln Val Val Lys Gly Gly Ala Phe Asp Gly

405

410

415

Thr Met Asn Gly Pro Phe Gly His Gly Tyr Gly Glu Gly Ala Gly Glu

420

425

430

Gly Ile His Asp Val Glu Trp Val Val Gly Lys Asp Lys Pro Thr Tyr

435

440

445

Asp Glu Ile Phe Tyr Thr Leu Ser Pro Val Asn Gly Lys Ile Thr Gly

450

455

460

Ala Asn Ala Lys Lys Glu Met Val Lys Ser Lys Leu Pro Asn Thr Val

465

470

475

480

Leu Gly Lys Ile Trp Lys Leu Ala Asp Val Asp Lys Asp Gly Leu Leu

485

490

495

Asp Asp Glu Glu Phe Ala Leu Ala Asn His Leu Ile Lys Val Lys Leu

500

505

510

Glu Gly His Glu Leu Pro Ala Asp Leu Pro Pro His Leu Val Pro Pro

515

520

525

Ser Lys Arg Arg His Glu

530

<210> 111

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<212> DNA

<213> Homo sapiens

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<222> (89).. (724)

<400> 111

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gigtgattaa cctccatttc agctaatac atg gga gag att aaa gtc tct cct 112

Met Gly Glu Ile Lys Val Ser Pro

1

5

gat tat aac tgg ttt aga ggt aca gtt ccc ctt aaa aag att att gtg 160

Asp Tyr Asn Trp Phe Arg Gly Thr Val Pro Leu Lys Lys Ile Ile Val

10	15	20	
gat gat gat gac agt aag ata tgg tgc ctc tat gac gcg ggc ccc cga			208
Asp Asp Asp Asp Ser Lys Ile Trp Ser Leu Tyr Asp Ala Gly Pro Arg			
25	30	35	40
agt atc agg tgt cct ctc ata ttc ctg ccc cct gtc agt gga act gca			256
Ser Ile Arg Cys Pro Leu Ile Phe Leu Pro Pro Val Ser Gly Thr Ala			
45	50	55	
gat gtc ttt ttc cgg cag att ttg gct ctg act gga tgg ggt tac cgg			304
Asp Val Phe Phe Arg Gln Ile Leu Ala Leu Thr Gly Trp Gly Tyr Arg			
60	65	70	
gtt atc gct ttg cag tat cca gtt tat tgg gac cat ctc gag ttc tgt			352
Val Ile Ala Leu Gln Tyr Pro Val Tyr Trp Asp His Leu Glu Phe Cys			
75	80	85	
gat gga ttc aga aaa ctt tta gac cat tta caa ttg gat aaa gtt cat			400
Asp Gly Phe Arg Lys Leu Leu Asp His Leu Gln Leu Asp Lys Val His			
90	95	100	
ctt ttt ggc gct tct ttg gga ggc ttt ttg gcc cag aaa ttt gct gaa			448
Leu Phe Gly Ala Ser Leu Gly Gly Phe Leu Ala Gln Lys Phe Ala Glu			
105	110	115	120
tac act cac aaa tct cct aga gtc cat tcc cta atc ctc tgc aat tcc			496
Tyr Thr His Lys Ser Pro Arg Val His Ser Leu Ile Leu Cys Asn Ser			
125	130	135	
ttc agt gac acc tct atc ttc aac caa act tgg act gca aac agc ttt			544
Phe Ser Asp Thr Ser Ile Phe Asn Gln Thr Trp Thr Ala Asn Ser Phe			
140	145	150	
tgg ctg atg cct gca ttt atg ctc aaa aaa ata gtt ctt gga aat ttt			592
Trp Leu Met Pro Ala Phe Met Leu Lys Lys Ile Val Leu Gly Asn Phe			

155	160	165	
tca tct ggc ccg gtg gac cct atg atg gct gat gcc att gat ttc atg	640		
Ser Ser Gly Pro Val Asp Pro Met Met Ala Asp Ala Ile Asp Phe Met			
170	175	180	
gta gac agg cta gaa agt ttg ggt cag agt gaa ctg gct tca aga ctt	688		
Val Asp Arg Leu Glu Ser Leu Gly Gln Ser Glu Leu Ala Ser Arg Leu			
185	190	195	200
acc ttg aaa ttg tca aaa ttc tta tgt gga acc tca taaaattcgg	734		
Thr Leu Lys Leu Ser Lys Phe Leu Cys Gly Thr Ser			
205	210		
ggacatacct gtaactatta tggatgtgtt tgatcagagt gcgctttcaa ctgaagctaa	794		
agaagaaatg tacaagctgt atccctaattg cccgaagag gctcatctga aaacaggagg	854		
caatttccca tacctgtgca gaagtgcaga ggtcaatctt tatgtacaga tacattttgc	914		
kgcaattccw kggrggacem aatacgcggc ctttgacceca tcaatggta gggccgagga	974		
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<211> 212

<212> PRT

<213> Homo sapiens

<400> 112

Met Gly Glu Ile Lys Val Ser Pro Asp Tyr Asn Trp Phe Arg Gly Thr

1 5 10 15

Val Pro Leu Lys Lys Ile Ile Val Asp Asp Asp Asp Ser Lys Ile Trp

20 25 30

Ser Leu Tyr Asp Ala Gly Pro Arg Ser Ile Arg Cys Pro Leu Ile Phe

35 40 45

Leu Pro Pro Val Ser Gly Thr Ala Asp Val Phe Phe Arg Gln Ile Leu

50 55 60

Ala Leu Thr Gly Trp Gly Tyr Arg Val Ile Ala Leu Gln Tyr Pro Val

65 70 75 80

Tyr Trp Asp His Leu Glu Phe Cys Asp Gly Phe Arg Lys Leu Leu Asp

85 90 95

His Leu Gln Leu Asp Lys Val His Leu Phe Gly Ala Ser Leu Gly Gly

100 105 110

Phe Leu Ala Gln Lys Phe Ala Glu Tyr Thr His Lys Ser Pro Arg Val

115 120 125

His Ser Leu Ile Leu Cys Asn Ser Phe Ser Asp Thr Ser Ile Phe Asn

130 135 140

Gln Thr Trp Thr Ala Asn Ser Phe Trp Leu Met Pro Ala Phe Met Leu

145 150 155 160

Lys Lys Ile Val Leu Gly Asn Phe Ser Ser Gly Pro Val Asp Pro Met

165 170 175

Met Ala Asp Ala Ile Asp Phe Met Val Asp Arg Leu Glu Ser Leu Gly

180

185

190

Gln Ser Glu Leu Ala Ser Arg Leu Thr Leu Lys Leu Ser Lys Phe Leu

195

200

205

Cys Gly Thr Ser

210

<210> 113

<211> 2391

<212> DNA

<213> Homo sapiens

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<223> g or t

<400> 113

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Asp Pro Phe His Ala Val Val Tyr Ile Val Phe Met Leu Gly Ser Cys

1

5

10

15

kcw tty kkc tcc aaa acg tgg att gag gtc tca ggt tcc tct scc aaa 96

Xaa Xaa Xaa Ser Lys Thr Trp Ile Glu Val Ser Gly Ser Ser Xaa Lys

20

25

30

gat gyt kca aag cag ctg aag gag cag cag atg gtg atg aga ggc cac 144

Asp Xaa Xaa Lys Gln Leu Lys Glu Gln Gln Met Val Met Arg Gly His

35

40

45

cga gag acc tcc atg gtc cat gaa ctc aac cgg tac atc ccc aca gcc 192

Arg Glu Thr Ser Met Val His Glu Leu Asn Arg Tyr Ile Pro Thr Ala

50

55

60

gcg gcc ttt ggt ggg ctg tgc atc ggg gcc ctc tcg gtc ctg gct gac 240

Ala Ala Phe Gly Gly Leu Cys Ile Gly Ala Leu Ser Val Leu Ala Asp
65 70 75 80
ttc cta ggc gcc att ggg tct gga acc ggg atc ctg ctc gca gtc aca 288
Phe Leu Gly Ala Ile Gly Ser Gly Thr Gly Ile Leu Leu Ala Val Thr
85 90 95
atc atc tac cag tac ttt gag atc ttc gtt aag gag yaa agc gag gtt 336
Ile Ile Tyr Gln Tyr Phe Glu Ile Phe Val Lys Glu Xaa Ser Glu Val
100 105 110
ggc agc atg ggg gcc ctg ctc ttc tgagcccgtc tcccggacag gttgaggaag 390
Gly Ser Met Gly Ala Leu Leu Phe
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<211> 120

<212> PRT

<213> Homo sapiens

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<223> unknown

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<400> 114

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1

5

10

15

Xaa Xaa Xaa Ser Lys Thr Trp Ile Glu Val Ser Gly Ser Ser Xaa Lys

20

25

30

Asp Xaa Xaa Lys Gln Leu Lys Glu Gln Gln Met Val Met Arg Gly His

35

40

45

Arg Glu Thr Ser Met Val His Glu Leu Asn Arg Tyr Ile Pro Thr Ala

50

55

60

Ala Ala Phe Gly Gly Leu Cys Ile Gly Ala Leu Ser Val Leu Ala Asp

65	70	75	80
Phe	Leu	Gly	Ala
Ile	Gly	Ser	Gly
Thr	Gly	Ile	Leu
Leu	Ala	Val	Thr
85	90	95	
Ile	Ile	Tyr	Gln
Tyr	Phe	Glu	Ile
Phe	Val	Lys	Glu
Xaa	Ser	Glu	Val
100	105	110	
Gly	Ser	Met	Gly
Ala	Leu	Leu	Phe
115	120		

<210> 115

<211> 599

<212> DNA

<213> Homo sapiens

<400> 115

gggataggaa ttggctgagg atcaaacgta ttaggtgaa aggataccag gatgttgcta 60
 aaggtgaggg acagtttggg ttgggacit accggggta tgtagatct ggaaccccca 120
 agtgaggctg gagggagtta aggtcagta ggaagatagg gtgggacag ggtgctttgg 180
 aatgaaagag tgacctaga gggctccttg ggcctcagga atgctcctgc tgcgtgaag 240
 atgagaaggt gctcttactc agttaatgat gaggactat attaccaaa gccctacct 300
 gctgctgggt ccttgtagc acaggagact tgggctaagg gcccctcca gggaaggac 360
 accatcaggc ctctggctga ggcagtagca tagaggatcc attctacct gcatttcca 420
 gaggactagc aggaggcagc ctgagaaac cggcagttcc caaagccagc gcctggctgt 480
 tctctattg tcactgcct ctcccaacc tctcctctaa ccactagag attgcctgtg 540
 tctgcctct tgcctcttgt agaatgcagc tctggccctc aataaatgt tctgcatt 599

<210> 116

<211> 364

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (134)

<223> a, c, g or t

<220>

<221> unsure

<222> (135)

<223> a, c, g or t

<220>

<221> unsure

<222> (179)

<223> g or a

<400> 116

ttcgaacaca tagttccctca tccccaccga agtgcatacaa atggcagtag aaatcactat 60

acagtgccttc caggggtgca ttgggtggaa tgagaatagt gatgaagtag aaatgtctgc 120

cacagttcca gganngggtg ggtagcagtg tgtgtgttat gtgccactga cctgaaara 180

tgtgccatag cccaagccaa ttgaaatga tcagggggcc aggcatggig gctcatgcct 240

glaatcccag caccttggga agctgaggtg ggaggattgc ttgaaaccag gatttcaaga 300

ccagcctgtg caacatagca aaaccccatc tctacaaaga tlaaaaataa aaaattagct 360

gggc

364

<210> 117

<211> 852

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (26).. (217)

<220>

<221> unsure

<222> (37)

<223> a, c, g or t

<400> 117

gttcagtttc aagtttaca gaggc atg gat gga gtn gtg acg ttc ttg aca 52

Met Asp Gly Xaa Val Thr Phe Leu Thr

1

5

agc tgg gct aac ctt tcc cga act tgt ttc ccg gag gca agg tgc tgc 100

Ser Trp Ala Asn Leu Ser Arg Thr Cys Phe Pro Glu Ala Arg Cys Ser

10

15

20

25

gtg acc cag cgc atc tta acc ttg ggt ctc cta ggc tgc agg cta ggg 148

Val Thr Gln Arg Ile Leu Thr Leu Gly Leu Leu Gly Ser Arg Leu Gly

30

35

40

cat tac gtt tgc tgg aac caa agc agc caa ttg cat agc aag tat ttt 196

His Tyr Val Ser Trp Asn Gln Ser Ser Gln Leu His Ser Lys Tyr Phe

45

50

55

cct gca ttc caa tta aat gct taagaaaaag cagcatccta taaaattgtg 247

Pro Ala Phe Gln Leu Asn Ala

60

atcataaaca tccatttccc tcagcttttg tgagtgcctt gacttacagc caacatcact 307
 gtttaactca gtcgttttaa aaacaaactt ttctgggtgt tgataacaga gatttgctcc 367
 ctgagccatc agggctcctgg gagctggaag tgaaagggtt attaacattc tacctttatg 427
 cagctgttgg ctgaccagaa taaactccct gctgagttca agctttgaat ggaatggatg 487
 caaatgatgt tgtttccatt agagcagggt ctcacagcat tctgattggc ctgagcagac 547
 cgaggctatg gctgttggga caagcttagc atcctggaca tcttgtcaaa gaacctcact 607
 caccctctg gcctctacag ccttcagagg agagaaaacc aattctccaa caaacaggtc 667
 tctccaacat ggtgggtctg gcaggcttag gtttagaaaa tctgactgt taaaggcgtt 727
 tgaatacatc acattcctat gcaaatgttt ttaatctcca gtttaatgia gtttattttt 787
 cctatatgta aagtattttt atacggcttg tatcatgata gtttagcaat aaaacagttg 847
 gaagc 852

<210> 118

<211> 64

<212> PRT

<213> Homo sapiens

<220>

<221> unsure

<222> (4)

<223> unknown

<400> 118

Met Asp Gly Xaa Val Thr Phe Leu Thr Ser Trp Ala Asn Leu Ser Arg

1

5

10

15

Thr Cys Phe Pro Glu Ala Arg Cys Ser Val Thr Gln Arg Ile Leu Thr

20

25

30

Leu Gly Leu Leu Gly Ser Arg Leu Gly His Tyr Val Ser Trp Asn Gln

35

40

45

Ser Ser Gln Leu His Ser Lys Tyr Phe Pro Ala Phe Gln Leu Asn Ala

50

55

60

<210> 119

<211> 1156

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (524).. (1105)

<220>

<221> unsure

<222> (10)

<223> a or t

<400> 119

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 gctagagaca gggagagcag agtaaaaccc tcaggcigct gaaatttcta ggctgttagg 180
 aagcccctcg aattctgtga aaatgagggt ttcttaactc acactgagag cggaaagggg 240
 cagacccttt tcataactcc ctcaagtgtg tgttaccttt ctttaccagc atggttaagca 300
 acaggacata tcccagcctc ggacatgtct gtatgatcca aggtacccaa agtcagacag 360
 agtaaaactca agcctggcac tggctttctg ccgcttcatg tgctttggaa aaagcaggag 420
 aagcaatagc agcaggagtc cccagcagct ggagccgcaa gaatgaactg caaagaggga 480
 actgacagca gcctcggctg cagggggcaa cgacgagaag aag atg ttg aag tgt 535

Met Leu Lys Cys

1

gtg gtg gtg ggg gac ggt gcc gtg ggg aaa acc tgc ctg ctg atg agc 583
 Val Val Val Gly Asp Gly Ala Val Gly Lys Thr Cys Leu Leu Met Ser
 5 10 15 20
 tac gcc aac gac gcc ttc cca gag gaa tac gtg ccc act gtg ttt gac 631
 Tyr Ala Asn Asp Ala Phe Pro Glu Glu Tyr Val Pro Thr Val Phe Asp
 25 30 35
 cac tat gca gtt act gtg act gtg gga ggc aag caa cac ttg ctc gga 679
 His Tyr Ala Val Thr Val Thr Val Gly Gly Lys Gln His Leu Leu Gly
 40 45 50
 ctg tat gac acc gcg gga cag gag gac tac aac cag ctg agg cca ctc 727
 Leu Tyr Asp Thr Ala Gly Gln Glu Asp Tyr Asn Gln Leu Arg Pro Leu
 55 60 65
 tcc tac ccc aac acg gat gtg ttt ttg atc tgc ttc tct gtc gta aac 775
 Ser Tyr Pro Asn Thr Asp Val Phe Leu Ile Cys Phe Ser Val Val Asn
 70 75 80
 cct gcc tct tac cac aat gtc cag gag gaa tgg gtc ccc gag ctc aag 823
 Pro Ala Ser Tyr His Asn Val Gln Glu Glu Trp Val Pro Glu Leu Lys
 85 90 95 100
 gac tgc atg cct cac gtg cct tat gtc ctc ata ggg acc cag att gat 871
 Asp Cys Met Pro His Val Pro Tyr Val Leu Ile Gly Thr Gln Ile Asp
 105 110 115
 ctc cgt gat gac cca aaa acc ttg gcc cgt ttg ctg tat atg aaa gag 919
 Leu Arg Asp Asp Pro Lys Thr Leu Ala Arg Leu Leu Tyr Met Lys Glu
 120 125 130
 aaa cct ctc act tac gag cat ggt gtg aag ctc gca aaa gcg atc gga 967
 Lys Pro Leu Thr Tyr Glu His Gly Val Lys Leu Ala Lys Ala Ile Gly

135 140 145
 gca cag tgc tac ttg gaa tgt tca gct ctg act cag aaa ggt ctc aaa 1015
 Ala Gln Cys Tyr Leu Glu Cys Ser Ala Leu Thr Gln Lys Gly Leu Lys
 150 155 160
 gcg gtt ttt gat gaa gca atc ctc acc att ttc cac ccc aag aaa aag 1063
 Ala Val Phe Asp Glu Ala Ile Leu Thr Ile Phe His Pro Lys Lys Lys
 165 170 175 180
 aag aaa cgc tgt tct gag ggt cac agc tgc tgt tca att atc 1105
 Lys Lys Arg Cys Ser Glu Gly His Ser Cys Cys Ser Ile Ile
 185 190
 tgagggtgtc tgggacctgc ctccacccca tccagggatg agaatggcag c 1156

<210> 120

<211> 194

<212> PRT

<213> Homo sapiens

<400> 120

Met Leu Lys Cys Val Val Val Gly Asp Gly Ala Val Gly Lys Thr Cys

1 5 10 15

Leu Leu Met Ser Tyr Ala Asn Asp Ala Phe Pro Glu Glu Tyr Val Pro

20 25 30

Thr Val Phe Asp His Tyr Ala Val Thr Val Thr Val Gly Gly Lys Gln

35 40 45

His Leu Leu Gly Leu Tyr Asp Thr Ala Gly Gln Glu Asp Tyr Asn Gln

50 55 60

Leu Arg Pro Leu Ser Tyr Pro Asn Thr Asp Val Phe Leu Ile Cys Phe

65 70 75 80

Ser Val Val Asn Pro Ala Ser Tyr His Asn Val Gln Glu Glu Trp Val
 85 90 95
 Pro Glu Leu Lys Asp Cys Met Pro His Val Pro Tyr Val Leu Ile Gly
 100 105 110
 Thr Gln Ile Asp Leu Arg Asp Asp Pro Lys Thr Leu Ala Arg Leu Leu
 115 120 125
 Tyr Met Lys Glu Lys Pro Leu Thr Tyr Glu His Gly Val Lys Leu Ala
 130 135 140
 Lys Ala Ile Gly Ala Gln Cys Tyr Leu Glu Cys Ser Ala Leu Thr Gln
 145 150 155 160
 Lys Gly Leu Lys Ala Val Phe Asp Glu Ala Ile Leu Thr Ile Phe His
 165 170 175
 Pro Lys Lys Lys Lys Lys Arg Cys Ser Glu Gly His Ser Cys Cys Ser
 180 185 190
 Ile Ile

<210> 121

<211> 1732

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (2).. (259)

<220>

<221> unsure

<222> (28)

<223> a, c, g or t

<220>

<221> unsure

<222> (388)

<223> g or a

<220>

<221> unsure

<222> (631)

<223> a or t

<220>

<221> unsure

<222> (637)

<223> g or a

<220>

<221> unsure

<222> (638)

<223> g or a

<220>

<221> unsure

<222> (639)

<223> g or a

<400> 121

g gac att gag tcc aag gag cag gtg cgn acc ctc acg ggc cac gtg ggc 49

Asp Ile Glu Ser Lys Glu Gln Val Xaa Thr Leu Thr Gly His Val Gly

1

5

10

15

acc gtg tat gcc ctg gcg gtc atc tcg acg cca gac cag acc aaa gtc 97

Thr Val Tyr Ala Leu Ala Val Ile Ser Thr Pro Asp Gln Thr Lys Val

20	25	30	
ttc agt gca tcc tac gac cgg tcc ctc agg gtc tgg agt atg gac aac	145		
Phe Ser Ala Ser Tyr Asp Arg Ser Leu Arg Val Trp Ser Met Asp Asn			
35	40	45	
atg atc tgc acg cag acc ctg ctg cgt cac cag ggc agt gtc acc gcg	193		
Met Ile Cys Thr Gln Thr Leu Leu Arg His Gln Gly Ser Val Thr Ala			
50	55	60	
ctg gct glg tcc cgg ggc cga ctc ttc tca ggg gct gtg gat agc act	241		
Leu Ala Val Ser Arg Gly Arg Leu Phe Ser Gly Ala Val Asp Ser Thr			
65	70	75	80
gtg aag gtt tgg act tgc taacaggatc caggccaggc tgtggtttcc	289		
Val Lys Val Trp Thr Cys			
85			
cctgaaccag ccttggacct ttctgagcca ggctggccac atgggggtgt ctcggggttt	349		
ctgcctgccc cgtgggcata ggtggacagg ctctggcarg ccggcagtc cctccccgtc	409		
ccatgctcgg cgagcctccc tctactcggc actgtccttg ctgcccagcc cctctctggg	469		
tgccaggtae gacgttggc ccggcccacc ctccatcccc accctccatc cccacctag	529		
atggagcgag ggcttttlla ctcacctttt ctaccgtttt tagactgtat gtagatttgg	589		
ttacctcttg gttgaaataa atgctccaca gactgtgaaa awaaaaarr acaamtccctc	649		
gggacaaggg ggctgtgtgt ggcttgagg ttggtgtgca caggcacttg ctgctgtgag	709		
tgggggggca tggggcagtt tcttttgggt gaccccagga cttcggccca ctccggggct	769		
ccccctcctg ctaggaggca actcgtcaca cccaagctgc tggcctccag tccatcctcc	829		
cccaacacat gtgccccaa aaagtgagcc aggcacctct gtttctgct gtttatlgac	889		
agccgacgga gcgccttggc cagacctccc ctgcccacct gctggagccc agcctgtgcc	949		
gccctctgag gagaggcctg gggggacagc tgggcacgtc cactcgcagg gaaacacggg	1009		
gtgagacagc aggaaggggc cctgcacgcc gggacgccac ctccgccagc cgctccacc	1069		
cgccccacac cacaatcgct ggttttcggc attttttaa tttttttt aagaaacgtc	1129		

aaagtgtgtgc ccaacactgt ggtacagcaa acacgataga ggagaccagt cagtacttct 1189
 tggaggggggc aggaggagag aggaaaaggg agggcgagaa tgaccacaca acacagcctt 1249
 ggaccaatgag cagaagcgtc cgtgggaact ccactgggtt ggtgggctg cctgcacagc 1309
 ccttgagag ggggccaggc acacctcag agggagctgc aagcccgigg cctggcctgc 1369
 tacatgccct gcttcacgt ggctgccacg ctgacacacc cacattcacc aaaccacacc 1429
 gcgccctggg acgcagccac gccaggagga ggacacggcc gccgagagca aggcacaacc 1489
 tcgagttctt ggggcgcaga gaacttagga gagaagcacg gaggagcccc cggcagagca 1549
 cccgcccccg ggccccagcc ttccacctgt gctagcagcc tggggcctcc actctggcgg 1609
 gaggaaggac cgcaggcaga cagcctgggc ctctaacagc tttgtccgg agctagactt 1669
 cgtgtccttt cagtlggtaa atggttttct atagaatcaa taatatttct ttctttaaat 1729
 ata 1732

<210> 122

<211> 86

<212> PRT

<213> Homo sapiens

<220>

<221> unsure

<222> (9)

<223> unknown

<400> 122

Asp Ile Glu Ser Lys Glu Gln Val Xaa Thr Leu Thr Gly His Val Gly

1

5

10

15

Thr Val Tyr Ala Leu Ala Val Ile Ser Thr Pro Asp Gln Thr Lys Val

20

25

30

Phe Ser Ala Ser Tyr Asp Arg Ser Leu Arg Val Trp Ser Met Asp Asn

35

40

45

Met Ile Cys Thr Gln Thr Leu Leu Arg His Gln Gly Ser Val Thr Ala

50

55

60

Leu Ala Val Ser Arg Gly Arg Leu Phe Ser Gly Ala Val Asp Ser Thr

65

70

75

80

Val Lys Val Trp Thr Cys

85

<210> 123

<211> 603

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (168).. (350)

<220>

<221> unsure

<222> (343)

<223> g or a

<220>

<221> unsure

<222> (422)

<223> t or c

<220>

<221> unsure

<222> (457)

<223> g or c

<400> 123

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 acagatglga cccaggccta ctaaagagac aactccacag ccttggaac acactcttga 120
 gccaaacttg gttgaagact aggtcttccc tggcaagttc cggaaga atg gac tta 176

Met Asp Leu

1

cig act ttt atc aac tct tct cac tgc caa ggc caa cag cat cig agg 224
 Leu Thr Phe Ile Asn Ser Ser His Cys Gln Gly Gln Gln His Leu Arg

5

10

15

tat agc ttt ttg gga gta cct gct ttc ttg cct cct gga gga tat ttt 272
 Tyr Ser Phe Leu Gly Val Pro Ala Phe Leu Pro Pro Gly Gly Tyr Phe

20

25

30

35

cig tcc tgg ggc ttc atg gcc cct ctc ttc cct gtt aca cat tgc tgt 320
 Leu Ser Trp Gly Phe Met Ala Pro Leu Phe Pro Val Thr His Cys Cys

40

45

50

gct tca gag cct ttg cag cig cra cct agt tgaatccaca taggsttcc 370
 Ala Ser Glu Pro Leu Gln Leu Xaa Pro Ser

55

60

tccacacggt gggaaggatc ttgctgcttt cactcacagg accaggaggat tyttcaatca 430
 ggagggtgggt ttttgttccc ttcaggscct tggcaacatc tagagacagt tttgattgcc 490
 acgectggag tgggatgtgt gtgctactgg catctagtgg ctgctaaaca tctacactg 550
 cataggatag tccccactac cccagccaa gaattatcig actccagggg tca 603

<210> 124

<211> 61

<212> PRT

<213> Homo sapiens

<220>

<221> unsure

<222> (59)

<223> unknown

<400> 124

Met Asp Leu Leu Thr Phe Ile Asn Ser Ser His Cys Gln Gly Gln Gln

1

5

10

15

His Leu Arg Tyr Ser Phe Leu Gly Val Pro Ala Phe Leu Pro Pro Gly

20

25

30

Gly Tyr Phe Leu Ser Trp Gly Phe Met Ala Pro Leu Phe Pro Val Thr

35

40

45

His Cys Cys Ala Ser Glu Pro Leu Gln Leu Xaa Pro Ser

50

55

60

<210> 125

<211> 1289

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (775).. (1017)

<220>

<221> unsure

<222> (200)

<223> g or a

<400> 125

tatgcgagcc aatattgaga gaggaatttt gctgaggttt tctctgaggt ttttttgatg 60

ctttatagga aactattttt taaaaaaagc catttccac ccaaggacac agtggatgtg 120

ttttccctga ctccagcagg gcaaggaatg taaccgagag gtigtgtggg ctgggctctg 180
 gtgccctctt ccttggcccr gaacacctct cctcctgalt cccttggcac ctgtctttc 240
 tgtctgttta cctgtctccc tgcctgccc a tctgcalctt ttgcagccca ctctgacttc 300
 catctggggg ctgagaccac ccttgccigc ccccttcttt ctgccctaaag aatgtccttt 360
 taggtggggc atgggtgtca cgccgtgaac ccagcactt tgggaggcgg agacgggcag 420
 alaacctgag gtcaggattt cgagaccaac ctgacctaca tggagaaact ccgctctag 480
 taaaaataca aaattagccg ggcatgggtg tgcacgcctc taatcccagc tactcgggag 540
 gctgaggcag gagaatcact tgaacccggg aagtggaggt tgcagtgagc caagagtaca 600
 ccactgcact ccagcctggg caacagagcg agactccgtc ttaaaaaaaaa aaaaaaaaaag 660
 aacgcccttt tactgtcttc atcatcccag tttaggcag tgcctggagtg gggaaggccg 720
 tcttagacca tagaggttgg aagacgtga gagatcatcc agcccagccc ctig atg 777

Met

1

tta cag agc aga aga cag atg ccc aaa cag gag aag gca ctt gcc cac 825
 Leu Gln Ser Arg Arg Gln Met Pro Lys Gln Glu Lys Ala Leu Ala His

5

10

15

ggt cat acg gca ggt tgc cac aaa acc aag atg gca gcc ctt cct cag 873
 Gly His Thr Ala Gly Cys His Lys Thr Lys Met Ala Ala Leu Pro Gln

20

25

30

cgt gcc tca ctg cca ctc cca gag cca ggg agc ccc ata aaa ccc aca 921
 Arg Ala Ser Leu Pro Leu Pro Glu Pro Gly Ser Pro Ile Lys Pro Thr

35

40

45

tca tgl ctt aag agt ata tct ggc tcc ttg acc agc aat cgg ccc tgg 969
 Ser Cys Leu Lys Ser Ile Ser Gly Ser Leu Thr Ser Asn Arg Pro Trp

50

55

60

65

gag cca cca ggt ggg aaa agc gcc tct gcc aga gtc cag gcc ttg gga 1017

Glu Pro Pro Gly Gly Lys Ser Ala Ser Ala Arg Val Gln Ala Leu Gly

70

75

80

tgacagacag cttgcccgca cactcgggcc ccactcaagg atglagggcc ttttctggcc 1077

cctgaccctt ccttgggcat tgggagcgtg gggacggggc tggccttggg aggagcggca 1137

ggggcatcac ctccctctgc tgcctcicc tgcctctacc ctcaagggcc tgggggctgc 1197

ccagctgcct ctatgccctt ctgggggtct cagccactg ctgacacttc tgcaatccag 1257

agaaacacta aataaagcaa tacgtgtttg cc

1289

<210> 126

<211> 81

<212> PRT

<213> Homo sapiens

<400> 126

Met Leu Gln Ser Arg Arg Gln Met Pro Lys Gln Glu Lys Ala Leu Ala

1

5

10

15

His Gly His Thr Ala Gly Cys His Lys Thr Lys Met Ala Ala Leu Pro

20

25

30

Gln Arg Ala Ser Leu Pro Leu Pro Glu Pro Gly Ser Pro Ile Lys Pro

35

40

45

Thr Ser Cys Leu Lys Ser Ile Ser Gly Ser Leu Thr Ser Asn Arg Pro

50

55

60

Trp Glu Pro Pro Gly Gly Lys Ser Ala Ser Ala Arg Val Gln Ala Leu

65

70

75

80

Gly

<210> 127

<211> 1085

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (734).. (886)

<220>

<221> unsure

<222> (276)

<223> g or t

<400> 127

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 ggaattacag gcacgcacca ccatgcctga ctaattttgt atttttagta gacatggggt 180
 ttctccatgt tggtcagget ggctcacaac tcccacctc agglgatccg cccacctcgg 240
 cctccigagg tggctgagat tacaggcgtg caactkgctc cagcttgcta attttcacag 300
 aagttgatgg caattcttca catgtaaaca gtgccagtgc acagaacctt tatatatit 360
 ttgaagccag tactgtgtc tcataataac aaagctgctt caaggatgag acctttttct 420
 aaaagcatgt aatgtgagaa gccggcctgc ctatatttct ttttctttt ttaatgatta 480
 aaaatagttt gtggcaaggc acggtggctc aggcctgtaa ttctagcact ttgggaggcc 540
 gaggcaggag gattacttga gcctacaagt ttgatgggcc agcatgcaca gcatagcaag 600
 actgcattct tacagagagt aaaaaaaaaa acccgagtgt ggtgatgtgc atctgtaac 660
 tcagctactt gggaggctga ggtgagagga tcacttgagc ttgggtgagg tgaggctgca 720
 gtgagtcctg atc atg ctg ctg cac tca atc ttg gac aac aga gca aga 769

Met Leu Leu His Ser Ile Leu Asp Asn Arg Ala Arg

1

5

10

ccc tgt ctg aaa aaa aaa aat ata tat ata tat ata tat tat ttt 817

Pro Cys Leu Lys Lys Lys Lys Asn Ile Tyr Ile Tyr Ile Tyr Tyr Phe

15

20

25

tat gag glg aag tgc atc aaa ctt ggg aaa gat ttg agg agg ctg gga 865

Tyr Glu Val Lys Cys Ile Lys Leu Gly Lys Asp Leu Arg Arg Leu Gly

30

35

40

acc tcc tgg aaa acc act cct tgaagaaaga tatgagagac atttagaagt 916

Thr Ser Trp Lys Thr Thr Pro

45

50

gattcctgct ttcagaagga ggtggattca aatacatcaa aagtccttc ctctgctaag 976

tgtttatagl tcaatgaata atttcaatat ttgtatgtgt tcttgtaatt ttattttttt 1036

ctgaaaaact tccaaaaatt tgaaaataaa attacagcct tttcttctt 1085

<210> 128

<211> 51

<212> PRT

<213> Homo sapiens

<400> 128

Met Leu Leu His Ser Ile Leu Asp Asn Arg Ala Arg Pro Cys Leu Lys

1

5

10

15

Lys Lys Lys Asn Ile Tyr Ile Tyr Ile Tyr Tyr Phe Tyr Glu Val Lys

20

25

30

Cys Ile Lys Leu Gly Lys Asp Leu Arg Arg Leu Gly Thr Ser Trp Lys

35

40

45

Thr Thr Pro

50

<210> 129

<211> 1544

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (1076)

<223> g or a

<400> 129

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ttgttaggaa ggatctggaa taatcttgaa gggaagtcag agttttctcc ctgcctatta 120

acaaaaaccc aattttgttc atattgaagc atgaaataaa tgagagcaag gtagggccaa 180

attaactctt gtggacagtc cctaaaagtc cagtcttaca ttgtgaaaa ttgtggtgcc 240

atgaattaag atggatgact ggaaaaaggt gttggagaaa gagttaaaga tgaggaagag 300

atatitttag tataatgaagt tatccaggga cttgalattc ataattcagt gctgtggaaa 360

tgaaaaaaat gattgaagag gtggaacgga aatgacctta gggggaaaaa aaaggaccaa 420

agaagtcctga ttaaaagttg aaatcagtat ttctgaattc aaattgcttg aatttccaaa 480

atagtcagta aaggatctaa tagaaccaga attatttggg tgaattctgc aggttttatg 540

ggcttgtcac aacgtgaagg gctggaatgt atattaccaa atgggaattt ccattgtagg 600

tttttgctag tcccaccccc attttagcct aatttggctt aaacgcagta tggggagaat 660

tgttcccatl ccaigtgttc tgaattcagc tcatctccca gcatatagat atatcctect 720

ttaactccga ccagaacctt tcttccigtg gcactcccca cccatagacc ttcagalcat 780

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ccttgccttt ctctacttcc aaatcacaat ttcttacaac caagctttgt gctcccgagt 900

aagcagggat gtactagggg aatgtaaaac tgcaaaactta aaaacctgca tcttcttgaa 960

gcalcagttt tacttlaccaa atggtttaga gtcataagat gacctatitt tatataaaag 1020

ttatattata gaataaaatg ttcatagca tagactgtta agataaaaaa ataggraatc 1080

ttgcaaggta attcttatit gcaagtggtt tatgtgttca ctctctctta cctttatggt 1140

attttgggtg tcacttacga agcatacaac tagaaccata tccaagcaga ctctgggttg 1200

ctgttaaccc agggcctaga ctcttagtgc ctctgaggca gaaccaaagg agcctgcact 1260

gggggaaatc ccttttctg cctgcctgtc tgccigtgac ctgtgtacgt attacaggct 1320

ttaggaccag ctgattgtta tgcttgcagg atggttttga aacagaaaca atacttgttt 1380

actgtaggaa tectatffat attatffffc aglcctgtga atgctgtgaa aagatttatt 1440

cctttgaggc caggaagctc ccaggcatat atgcttctag gttaggattg tectgactca 1500

ctaaagatgc caggatattg gggctgaggg gagtttgagg tgit 1544

<210> 130

<211> 508

<212> DNA

<213> Homo sapiens

<400> 130

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atgggaaaca ggttatcggg ggattcatga agtcagtga agtaattgct tcttttttgc 120

gggtgaactg aatgtatttc ttacacaaat ctgatgtta acaattaaaa agaagaaatg 180

acatgcaagt aggtcttagc agaaaaatgc aggcctgggca tgagtcatgt tgitaccctc 240

ccacatgctc ctacaatcca cagagatgcc tgtctgcagg ttcttgaagt tatgttagt 300

atttggatc tcaaattttt cgtcactgtt cacatgccac ttctctgtg cacagtggta 360

tcctcattg ctttttaacc tacactgagg agtccttgc aggttgcaat gattttccaa 420

ttctgcagta atgagtaagc tcacggcatg gggaagaaga cagtcagtc aatgaagttc 480

tcctaaattat tttaacattg cctttgaa

508

<210> 131

<211> 1204

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (50)

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<220>

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<222> (54)

<223> g or c

<220>

<221> unsure

<222> (300)

<223> g or c

<220>

<221> unsure

<222> (407)

<223> g or a

<220>

<221> unsure

<222> (415)

<223> a, c, g or t

<220>

<221> unsure

<222> (417)

<223> g or c

<220>

<221> unsure

<222> (419)

<223> t or c

<220>

<221> unsure

<222> (430)

<223> a or t

<220>

<221> unsure

<222> (448)

<223> t or c

<220>

<221> unsure

<222> (449)

<223> g or t

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<221> unsure

<222> (472)

<223> a, c, g or t

<400> 131

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gtggccacc ttgggtcag acagctctgg gccctttgac cacaagccag cccctgccc 180

tctcttggtc atagtctct ctgcccagg actgcaggc ggcttctcc aaggcttcca 240

aggctcaaaa gaaatttggc tccatccaag aaggctccag ctcccctact ggccctggs 300

ttcaggccca ccccttggg ccagggccag agagtgtgc tcaggagaat tcaatgggt 360

ctagagagac acacagaaag ttgggcatt tgggaaatt tcaaggrgt atgntsgyt 420

cacgtatggw gcaggttgc ctggtccykg ggtgcaggga agtgggtgc anggaagtg 480

attggagggg agcttgagga atataaggag cgggggtgga gactcaggct atggacaagg 540

acagcccaa ggttgggaag acctggcctt agtcgtctc agcctagggg cagggcagt 600

aagaaagctc tccccgtcc tgcgtaatg acccagagta gccctcccag gccggcatct 660

tatgtgtgc ttccaccat ctcattgttg cactttcta ggctgtctc ccagcattgt 720

gcaaggctcg gaagagaacc aggaagtga aactgggtga aaacagaaag ctcaatgat 780

gggctagggt ccccgatca ttagggcaga gtttgcacgt cctctggta ctggaatcca 840

cccagccac gaatcaatc cctctgaag gatattttt ctactgggt ttggaacaaa 900

ctcctgctga gacccacag ccagaaactg aaagcagcag ctcccaaag cctggaaaat 960

ccctaagaga aggcctgggg caggaagtgg agtgacagg gacaggtaga gagaagggg 1020

cccaatggcc agggagtga ggaggtggcg ttgctgagag cagctgcac atgtttctgt 1080

ctgagtgcag gaaggtgtc cagggtcga attacactt tctacctgg agacgtgtt 1140

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cctg 1204

<210> 132

<211> 508

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (223)

<223> a, c, g or t

<220>

<221> unsure

<222> (237)

<223> a, c, g or t

<220>

<221> unsure

<222> (380)

<223> a, c, g or t

<220>

<221> unsure

<222> (468)

<223> a, c, g or t

<400> 132

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acactccagc ctgggtgaca gagtgagatc ctgctcctaaa aaaagagaaa gaaaaccttt 120

gagattcttc catTTTTaga gctgagagag cacttgigaa acacacacac atgcacaaac 180

atataaacat gcatacaggc atgcacatgc acacacaaat acncatacac acacacnagc 240

acacacacac caccaccacc atcatcagag gaacttacag aaaaggggac atttatagat 300

tcttaggaat atgccaaagc ttttcaaagc ctctatggac agctcatlcc ttaacttttc 360

ctcttttaaaa tctttttttan cttcttattt gccccagcca ctatcacatgc ctgaggcagc 420

tgcaacgtta aacaattgcc actgattact ttcaacaaat aacctcanag aaaaggctgt 480

gtgtattgaa tgggtatcaa gtcacgtc

508

<210> 133

<211> 484

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (313)

<223> a, c, g or t

<220>

<221> unsure

<222> (336)

<223> g or c

<220>

<221> unsure

<222> (401)

<223> g or c

<400> 133

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tcttggagag ggaaggagac tgaagagtga gtttggtcct ccacttgatc caggttctta 120

tttttgtttt ctacttcaaa gcgagaactt ggtactgtga ctttgataag aattgacttc 180

aggcccagca agatccctca tgcctgtaat cccagcactt tggggggcca aggcaggagg 240

attgcgtgag cccaggagtt cgagaccac ctgggcaaca tagggacctt gtctctacaa 300

aaaataaaat tancctgggtt tgatgglgca catcastggt cctggctact cgggaggcca 360

aggtagggagg aatgcttgag gatcggaggt caaggctgca stgagccaat attgtgccac 420

tgcatccag cctgggcaac agagttagac actgtcttaa aaaaaaaaaa aaaaaacggt 480

ccgc 484

<210> 134

<211> 605

<212> DNA

<213> Homo sapiens

<400> 134

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ggaatttgag ttctctctaa cccagcttac tgtgggacat aggaaaactc agtagaaata 180

cccttgggtga tcttgttgag ttttaagctg atcttgatct taaactcagt aagccactat 240

ctgcaatttt gtacattata tagtatcttg aagataigga accttatgaa aaaaaaatag 300

caaattagtt ctttttcccc cagaggggaa agttaatgtc tgcaaatagt gtgtgtctta 360

ttttactggt gaacagcaat tgctatttat ttttttatig cctagaactt caacatgttg 420

tataggaatc ctgtatgcc actagttaaa tgccgaattc tcatctggat gttaccatca 480

aacatcaglia cacttgteat ttacatgtg tttaatgiga cagtttttca gtactglatg 540

tgtaatttc tacttttttt aatatttaaa attgctttta aataaacata ttctcagttg 600

atccc 605

<210> 135

<211> 1786

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (2).. (151)

<220>

<221> unsure

<222> (689)

<223> g or a

<400> 135

g gca cga ggg tcc tct gca tgg ggt cag gtg ctt ctg tgc ttg ctg tcc 49

Ala Arg Gly Ser Ser Ala Trp Gly Gln Val Leu Leu Cys Leu Leu Ser

1

5

10

15

tac ctc tct cca cag cag ggc tct caa aac cat ttt gat ccc cca ttg 97

Tyr Leu Ser Pro Gln Gln Gly Ser Gln Asn His Phe Asp Pro Pro Leu

20

25

30

gca gag ggt tcc cct ctt tac aga gtt cag tca tta aaa gca tgg atc 145

Ala Glu Gly Ser Pro Leu Tyr Arg Val Gln Ser Leu Lys Ala Trp Ile

35

40

45

agc tgt taatctcatt ggaggaggga acigtctcct gcattcatt atctgggaac 201

Ser Cys

50

cttcttgagt agccactgtc tgcagccac tgctctagag atgggaaaac agcacggaac 261

aaaaccaagg tctttcttcc agcgaattta tatcttcag gaagctggttcctgccacca 321

acttagcagg caacagttct cctcccctag tgggcacagg gtaccagttt ttaggaaaa 381

gtggctcagc aaaggaagaa agcagaccaa cccagctgcc ttaccttatt ctggggccat 441

tccccagcg atgagagctg ctcttgttc tactgccacc atctctctg gctgcattc 501

acctgctgct tgagctctg accttcctc agttccacca aatgaggaca ggaaatagca 561

gtcaagacc ctgggccctg ctgagcgtga aacaggaagg caatgggatg agttgctggg 621

acggaagaat gggcctgggg cagaacaaat agggagcatt tgaagcttc tggctgataa 681

atctccargg tgcctccgg ttgccagcc tgccccatt aacctgctcc tggtaaatac 741

tgatccagca gctgctccag gagaggcct ctttttttc ccagccagc tgtgtctttg 801

catgagactc cttggggcct gggcacagag agaaaagaat tgagactcag gaggtcagt 861

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acttgggaga tgaacttcag ggccttcga cgccttgtct caggaacatg ctttggagaa 981

aatggtagca tctttccat aactcagtct ctcttcccta gtctccctga agtgtgacgt 1041

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gcctccacc aataagcaaa ctggagattc ctacgctct ctgggacacc cacatctcat 1221

tcttctcaca gcagagaagc tcctcccttca gccctgagctg tcttctttct gctgcagtgc 1281
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 tcttacttll gacttatttg gccctcatct tggcatggaa ggctggcaggc agaattgaaa 1401
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 ctatcccatg agactagggg ccggagccca ccctgccttc cccacaactt ttctgtctca 1521
 aaccactcc tcttgacaca ctggaatctg tattatata attttaaga aaatacaatg 1581
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 agtatttaaa atgttccaat aaagtggggt ttttgttat tctaataat tatttgttac 1701
 ctattgtaaa tatgaaacac tcctattttg caagctgagg acacaatttg tactgttgtt 1761
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<210> 136

<211> 50

<212> PRT

<213> Homo sapiens

<400> 136

Ala Arg Gly Ser Ser Ala Trp Gly Gln Val Leu Leu Cys Leu Leu Ser

1

5

10

15

Tyr Leu Ser Pro Gln Gln Gly Ser Gln Asn His Phe Asp Pro Pro Leu

20

25

30

Ala Glu Gly Ser Pro Leu Tyr Arg Val Gln Ser Leu Lys Ala Trp Ile

35

40

45

Ser Cys

50

<210> 137

<211> 835

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (535).. (729)

<400> 137

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 agaacctcaa ttgacattcc ttggaatagg ctaataagtg acaaataaga ttaataagat 180
 ttttcaaaat cgccaggact ggtgaatata aatgatgatt gaactggaat aatattgggg 240
 accaaatcaa atgaatgatt aaattatgaa gtcataatcc ttttgaaggt agttgcaaag 300
 agacatttca aaactgccct aggccattgc agcatcctta galgggacgc ataataatta 360
 ccttaaagca tcaccactca ttttgaccat atagatttta ttatgttagt ttaaaaggtc 420
 aatcagcctc atgacittat agttaatgct tgtattttaa aacatttttt atacatttgg 480
 ttatgttgat aaacaaaaaa catttgatta ataaaatata tatttgaata aatt atg 537

Met

1

agc tat cct ttc aaa cag cta ttg gca agt ttt aaa ccc aaa ata tat 585

Ser Tyr Pro Phe Lys Gln Leu Leu Ala Ser Phe Lys Pro Lys Ile Tyr

5

10

15

aca cat agt tct gta ata aaa ctg ttt gac ttc tca agt aac atg act 633

Thr His Ser Ser Val Ile Lys Leu Phe Asp Phe Ser Ser Asn Met Thr

20

25

30

tcc tta ttt ctg aac agt act ggt tac ttt caa aat gaa ttt tta ttg 681

Ser Leu Phe Leu Asn Ser Thr Gly Tyr Phe Gln Asn Glu Phe Leu Leu

35

40

45

aga ttt tcc att aac tat ttt ttt caa aga ctc aaa ttt tgt acc aag 729

Arg Phe Ser Ile Asn Tyr Phe Phe Gln Arg Leu Lys Phe Cys Thr Lys

50

55

60

65

taaatccagg ctttaagtac aaacatgttg ttgttttat ttggggctgg gggaggata 789

tgaatgagcag acttctcgga attcataata aattttctaa aagcct

835

<210> 138

<211> 65

<212> PRT

<213> Homo sapiens

<400> 138

Met Ser Tyr Pro Phe Lys Gln Leu Leu Ala Ser Phe Lys Pro Lys Ile

1

5

10

15

Tyr Thr His Ser Ser Val Ile Lys Leu Phe Asp Phe Ser Ser Asn Met

20

25

30

Thr Ser Leu Phe Leu Asn Ser Thr Gly Tyr Phe Gln Asn Glu Phe Leu

35

40

45

Leu Arg Phe Ser Ile Asn Tyr Phe Phe Gln Arg Leu Lys Phe Cys Thr

50

55

60

Lys

65

<210> 139

<211> 626

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) .. (201)

<220>

<221> unsure

<222> (348)

<223> t or c

<220>

<221> unsure

<222> (353)

<223> a or t

<220>

<221> unsure

<222> (358)

<223> a or t

<220>

<221> unsure

<222> (363)

<223> a or t

<220>

<221> unsure

<222> (368)

<223> g or a

<400> 139

tgt ttc agt gtg act gtc ttg tta gag gtg aag ttt atc cag ggt aac 48

Cys Phe Ser Val Thr Val Leu Leu Glu Val Lys Phe Ile Gln Gly Asn

1

5

10

15

ttg ctc act aac tat tcc ttt tta tgg cct ggg gtt aaa ggg agc atg 96

Leu Leu Thr Asn Tyr Ser Phe Leu Trp Pro Gly Val Lys Gly Ser Met

20

25

30

gct cac act ggt gaa aat aag gaa ggc ctg gtc tta tct tgt att aat 144

Ala His Thr Gly Glu Asn Lys Glu Gly Leu Val Leu Ser Cys Ile Asn

35

40

45

aat act ggc tgc att cca cca gcc aga gat ttc tat ctg cga aga cct 192

Asn Thr Gly Cys Ile Pro Pro Ala Arg Asp Phe Tyr Leu Arg Arg Pro

50

55

60

atg aaa cac tgaagagaaa tgtaggcaga aggaaatggc cacatacac 241

Met Lys His

65

aagtcttatt atatatcttt ttgtaaatac atattgtata ttacttggat gttttcttat 301

atcatttact gtctttttga gttaatgtca gtttttactc tctcaaytta cwatgtwaca 361

twgtaartaa cataatgtcc ttatattttt atatttaagc atctaacata tagagtttgt 421

ttcatataag tttaagataa atgtcaaaaa tataatgttct ttgttttttc ttgtctttaa 481

aattatgtat cttttccttt tctttttttt aagaataatt tatgtttcag gagaaagaat 541

gtataatgtaa ctgaaactat ctgaagaatg cacattgaag gccgtgaggt actgataaac 601

taaagaattt attattcaaa atact 626

<210> 140

<211> 67

<212> PRT

<213> Homo sapiens

<400> 140

Cys Phe Ser Val Thr Val Leu Leu Glu Val Lys Phe Ile Gln Gly Asn

1

5

10

15

Leu Leu Thr Asn Tyr Ser Phe Leu Trp Pro Gly Val Lys Gly Ser Met

20 25 30
 Ala His Thr Gly Glu Asn Lys Glu Gly Leu Val Leu Ser Cys Ile Asn
 35 40 45
 Asn Thr Gly Cys Ile Pro Pro Ala Arg Asp Phe Tyr Leu Arg Arg Pro
 50 55 60
 Met Lys His
 65

<210> 141

<211> 525

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (103).. (525)

<400> 141

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 tcactctggt aaagctggtc tgttctaact gagatgacag tc atg tcc ctt tcc 114

Met Ser Leu Ser

1

agg gac ctc aag gac gac ttt cac agt gac acg gla ctc tcc atc tta 162

Arg Asp Leu Lys Asp Asp Phe His Ser Asp Thr Val Leu Ser Ile Leu

5 10 15 20

aat gag cag cgc att cgg ggc att tta tgc gat gtc act atc att gtg 210

Asn Glu Gln Arg Ile Arg Gly Ile Leu Cys Asp Val Thr Ile Ile Val

25 30 35

gaa gat acc aaa ttt aaa gcc cat agc aat gtt ctg gca gct tca agc 258

Glu Asp Thr Lys Phe Lys Ala His Ser Asn Val Leu Ala Ala Ser Ser
 40 45 50
 ctg tat ttt aaa aat atc ttt tgg agc cat aca atc tgt att tcc agc 306
 Leu Tyr Phe Lys Asn Ile Phe Trp Ser His Thr Ile Cys Ile Ser Ser
 55 60 65
 cac gtc ctg gag ctg gac gat ctc aaa gct gaa gtg ttt act gaa ata 354
 His Val Leu Glu Leu Asp Asp Leu Lys Ala Glu Val Phe Thr Glu Ile
 70 75 80
 ctt aat tat atc tac agt tcc aca gtc gtt gtc aag aga cag gaa aca 402
 Leu Asn Tyr Ile Tyr Ser Ser Thr Val Val Val Lys Arg Gln Glu Thr
 85 90 95 100
 gtc act gat ctc gca gct gca gga aaa aag ctg gga ata tcg ttc ttg 450
 Val Thr Asp Leu Ala Ala Ala Gly Lys Lys Leu Gly Ile Ser Phe Leu
 105 110 115
 gaa gac ctt act gat cgc aac ttc tca aat tcc ccg ggt ccc tat gla 498
 Glu Asp Leu Thr Asp Arg Asn Phe Ser Asn Ser Pro Gly Pro Tyr Val
 120 125 130
 ttc tgt att act gaa aag gga gtg gtt 525
 Phe Cys Ile Thr Glu Lys Gly Val Val
 135 140

<210> 142

<211> 141

<212> PRT

<213> Homo sapiens

<400> 142

Met Ser Leu Ser Arg Asp Leu Lys Asp Asp Phe His Ser Asp Thr Val

1	5	10	15
Leu Ser Ile Leu Asn Glu Gln Arg Ile Arg Gly Ile Leu Cys Asp Val			
20	25	30	
Thr Ile Ile Val Glu Asp Thr Lys Phe Lys Ala His Ser Asn Val Leu			
35	40	45	
Ala Ala Ser Ser Leu Tyr Phe Lys Asn Ile Phe Trp Ser His Thr Ile			
50	55	60	
Cys Ile Ser Ser His Val Leu Glu Leu Asp Asp Leu Lys Ala Glu Val			
65	70	75	80
Phe Thr Glu Ile Leu Asn Tyr Ile Tyr Ser Ser Thr Val Val Val Lys			
85	90	95	
Arg Gln Glu Thr Val Thr Asp Leu Ala Ala Ala Gly Lys Lys Leu Gly			
100	105	110	
Ile Ser Phe Leu Glu Asp Leu Thr Asp Arg Asn Phe Ser Asn Ser Pro			
115	120	125	
Gly Pro Tyr Val Phe Cys Ile Thr Glu Lys Gly Val Val			
130	135	140	

<210> 143

<211> 1827

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (138).. (1307)

<400> 143

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 cccggccagg gagggcc atg att tcc ctc ccg ggg ccc ctg gtg acc aac 170
 Met Ile Ser Leu Pro Gly Pro Leu Val Thr Asn
 1 5 10
 ttg ctg cgg ttt ttg ttc ctg ggg ctg agt gcc ctc gcg ccc ccc teg 218
 Leu Leu Arg Phe Leu Phe Leu Gly Leu Ser Ala Leu Ala Pro Pro Ser
 15 20 25
 cgg gcc cag ctg caa ctg cac ttg ccc gcc aac cgg ttg cag gcg gtg 266
 Arg Ala Gln Leu Gln Leu His Leu Pro Ala Asn Arg Leu Gln Ala Val
 30 35 40
 gag gga ggg gaa gtg gtg ctt cca gcg tgg tac acc ttg cac ggg gag 314
 Glu Gly Gly Glu Val Val Leu Pro Ala Trp Tyr Thr Leu His Gly Glu
 45 50 55
 gtg tct tca tcc cag cca tgg gag gtg ccc ttt gtg atg tgg ttc ttc 362
 Val Ser Ser Ser Gln Pro Trp Glu Val Pro Phe Val Met Trp Phe Phe
 60 65 70 75
 aaa cag aaa gaa aag gag gat cag gtg ttg tcc tac atc aat ggg gtc 410
 Lys Gln Lys Glu Lys Glu Asp Gln Val Leu Ser Tyr Ile Asn Gly Val
 80 85 90
 aca aca agc aaa cct gga gla tcc ttg gtc tac tcc atg ccc tcc cgg 458
 Thr Thr Ser Lys Pro Gly Val Ser Leu Val Tyr Ser Met Pro Ser Arg
 95 100 105
 aac ctg tcc ctg cgg ctg gag ggt ctc cag gag aaa gac tct ggc ccc 506
 Asn Leu Ser Leu Arg Leu Glu Gly Leu Gln Glu Lys Asp Ser Gly Pro
 110 115 120
 tac agc tgc tcc gtg aat gtg caa gac aaa caa ggc aaa tct agg ggc 554
 Tyr Ser Cys Ser Val Asn Val Gln Asp Lys Gln Gly Lys Ser Arg Gly

125	130	135	
cac agc atc aaa acc tta gaa ctc aat gta ctg gtt cct cca gct cct			602
His Ser Ile Lys Thr Leu Glu Leu Asn Val Leu Val Pro Pro Ala Pro			
140	145	150	155
cca tcc tgc cgt ctc cag ggt gtg ccc cat gtg ggg gca aac gtg acc			650
Pro Ser Cys Arg Leu Gln Gly Val Pro His Val Gly Ala Asn Val Thr			
160	165	170	
ctg agc tgc cag tct cca agg agt aag cct gct gtc caa tac cag tgg			698
Leu Ser Cys Gln Ser Pro Arg Ser Lys Pro Ala Val Gln Tyr Gln Trp			
175	180	185	
gat cgg cag ctt cca tcc ttc cag act ttc ttt gca cca gca tta gat			746
Asp Arg Gln Leu Pro Ser Phe Gln Thr Phe Phe Ala Pro Ala Leu Asp			
190	195	200	
gtc atc cgt ggg tct tta agc ctc acc aac ctt tgc tct tcc atg gct			794
Val Ile Arg Gly Ser Leu Ser Leu Thr Asn Leu Ser Ser Ser Met Ala			
205	210	215	
gga gtc tat gtc tgc aag gcc cac aat gag gtg ggc act gcc caa tgt			842
Gly Val Tyr Val Cys Lys Ala His Asn Glu Val Gly Thr Ala Gln Cys			
220	225	230	235
aat gtg acg ctg gaa gtg agc aca ggg cct gga gct gca gtg gtt gct			890
Asn Val Thr Leu Glu Val Ser Thr Gly Pro Gly Ala Ala Val Val Ala			
240	245	250	
gga gct gtt gtg ggt acc ctg gtt gga ctg ggg ttg ctg gct ggg ctg			938
Gly Ala Val Val Gly Thr Leu Val Gly Leu Gly Leu Leu Ala Gly Leu			
255	260	265	
gtc ctc ttg tac cac cgc cgg ggc aag gcc ctg gag gag cca gcc aat			986

Val Leu Leu Tyr His Arg Arg Gly Lys Ala Leu Glu Glu Pro Ala Asn

270

275

280

gat atc aag gag gat gcc att gct ccc cgg acc ctg ccc tgg ccc aag 1034

Asp Ile Lys Glu Asp Ala Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys

285

290

295

agc tca gac aca atc tcc aag aat ggg acc ctt tcc tct gtc acc tcc 1082

Ser Ser Asp Thr Ile Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser

300

305

310

315

gca cga gcc ctc tgg cca ccc cal ggc cct ccc agg cct ggt gca ttg 1130

Ala Arg Ala Leu Trp Pro Pro His Gly Pro Pro Arg Pro Gly Ala Leu

320

325

330

acc ccc acg ccc agt ctc tcc agc cag gcc ctg ccc tca cca aga ctg 1178

Thr Pro Thr Pro Ser Leu Ser Ser Gln Ala Leu Pro Ser Pro Arg Leu

335

340

345

ccc acg aca gat ggg gcc cac cct caa cca ata tcc ccc atc cct ggt 1226

Pro Thr Thr Asp Gly Ala His Pro Gln Pro Ile Ser Pro Ile Pro Gly

350

355

360

ggg gtt tct tcc tct ggc ttg agc cgc atg ggt gct gtg cct gtg atg 1274

Gly Val Ser Ser Ser Gly Leu Ser Arg Met Gly Ala Val Pro Val Met

365

370

375

gtg cct gcc cag agt caa gct ggc tct ctg gta tgatgacccc accactcatt 1327

Val Pro Ala Gln Ser Gln Ala Gly Ser Leu Val

380

385

390

ggctaaagga ttgggggtct ctcttctcta taagggtcac ctctagcaca gaggcctgag 1387

tcatgggaaa gagtcacact cctgacctt agtactctgc cccacctct cttactgtg 1447

ggaaaacat ctacagtaaga cctaagtgtc caggagacag aaggagaaga ggaagtggat 1507

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<210> 144

<211> 390

<212> PRT

<213> Homo sapiens

<400> 144

Met Ile Ser Leu Pro Gly Pro Leu Val Thr Asn Leu Leu Arg Phe Leu

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Phe Leu Gly Leu Ser Ala Leu Ala Pro Pro Ser Arg Ala Gln Leu Gln

20 25 30

Leu His Leu Pro Ala Asn Arg Leu Gln Ala Val Glu Gly Gly Glu Val

35 40 45

Val Leu Pro Ala Trp Tyr Thr Leu His Gly Glu Val Ser Ser Ser Gln

50 55 60

Pro Trp Glu Val Pro Phe Val Met Trp Phe Phe Lys Gln Lys Glu Lys

65 70 75 80

Glu Asp Gln Val Leu Ser Tyr Ile Asn Gly Val Thr Thr Ser Lys Pro

85 90 95

Gly Val Ser Leu Val Tyr Ser Met Pro Ser Arg Asn Leu Ser Leu Arg

100 105 110

Leu Glu Gly Leu Gln Glu Lys Asp Ser Gly Pro Tyr Ser Cys Ser Val

115 120 125

Asn Val Gln Asp Lys Gln Gly Lys Ser Arg Gly His Ser Ile Lys Thr
 130 135 140
 Leu Glu Leu Asn Val Leu Val Pro Pro Ala Pro Pro Ser Cys Arg Leu
 145 150 155 160
 Gln Gly Val Pro His Val Gly Ala Asn Val Thr Leu Ser Cys Gln Ser
 165 170 175
 Pro Arg Ser Lys Pro Ala Val Gln Tyr Gln Trp Asp Arg Gln Leu Pro
 180 185 190
 Ser Phe Gln Thr Phe Phe Ala Pro Ala Leu Asp Val Ile Arg Gly Ser
 195 200 205
 Leu Ser Leu Thr Asn Leu Ser Ser Ser Met Ala Gly Val Tyr Val Cys
 210 215 220
 Lys Ala His Asn Glu Val Gly Thr Ala Gln Cys Asn Val Thr Leu Glu
 225 230 235 240
 Val Ser Thr Gly Pro Gly Ala Ala Val Val Ala Gly Ala Val Val Gly
 245 250 255
 Thr Leu Val Gly Leu Gly Leu Leu Ala Gly Leu Val Leu Leu Tyr His
 260 265 270
 Arg Arg Gly Lys Ala Leu Glu Glu Pro Ala Asn Asp Ile Lys Glu Asp
 275 280 285
 Ala Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys Ser Ser Asp Thr Ile
 290 295 300
 Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser Ala Arg Ala Leu Trp
 305 310 315 320
 Pro Pro His Gly Pro Pro Arg Pro Gly Ala Leu Thr Pro Thr Pro Ser
 325 330 335

Leu Ser Ser Gln Ala Leu Pro Ser Pro Arg Leu Pro Thr Thr Asp Gly

340

345

350

Ala His Pro Gln Pro Ile Ser Pro Ile Pro Gly Gly Val Ser Ser Ser

355

360

365

Gly Leu Ser Arg Met Gly Ala Val Pro Val Met Val Pro Ala Gln Ser

370

375

380

Gln Ala Gly Ser Leu Val

385

390

<210> 145

<211> 3466

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (84).. (2726)

<400> 145

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gggccgccgc cgccaccgcc gcc atg aag aag cag ttc aac cgc atg aag cag 113

Met Lys Lys Gln Phe Asn Arg Met Lys Gln

1

5

10

ctg gct aac cag acc gtg ggc aga gct gag aaa aca gaa gtc ctt agt 161

Leu Ala Asn Gln Thr Val Gly Arg Ala Glu Lys Thr Glu Val Leu Ser

15

20

25

gaa gat cta tta cag att gag aga cgc ctg gac acg gtg cgg tca ata 209

Glu Asp Leu Leu Gln Ile Glu Arg Arg Leu Asp Thr Val Arg Ser Ile

30

35

40

tgc cac cat tcc cat aag cgc ttg gtg gca tgt ttc cag ggc cag cat 257

Cys His His Ser His Lys Arg Leu Val Ala Cys Phe Gln Gly Gln His

45

50

55

ggc acc gat gcc gag agg aga cac aaa aaa ctg cct ctg aca gct ctt 305

Gly Thr Asp Ala Glu Arg Arg His Lys Lys Leu Pro Leu Thr Ala Leu

60

65

70

gct caa aat atg caa gaa gca tgc act cag ctg gaa gac tct ctc ctg 353

Ala Gln Asn Met Gln Glu Ala Ser Thr Gln Leu Glu Asp Ser Leu Leu

75

80

85

90

ggg aag atg ctg gag acg tgt gga gat gct gag aat cag ctg gct ctc 401

Gly Lys Met Leu Glu Thr Cys Gly Asp Ala Glu Asn Gln Leu Ala Leu

95

100

105

gag ctc tcc cag cac gaa gtc ttt gtt gag aag gag atc gtg gac cct 449

Glu Leu Ser Gln His Glu Val Phe Val Glu Lys Glu Ile Val Asp Pro

110

115

120

ctg tac ggc ata gct gag gtg gag att ccc aac atc cag aag cag agg 497

Leu Tyr Gly Ile Ala Glu Val Glu Ile Pro Asn Ile Gln Lys Gln Arg

125

130

135

aag cag ctt gca aga ttg gtg tta gac tgg gat tca gtc aga gcc agg 545

Lys Gln Leu Ala Arg Leu Val Leu Asp Trp Asp Ser Val Arg Ala Arg

140

145

150

tgg aac caa gct cac aaa tcc tca gga acc aac ttt cag ggg ctt cca 593

Trp Asn Gln Ala His Lys Ser Ser Gly Thr Asn Phe Gln Gly Leu Pro

155

160

165

170

tca aaa ata gat act cta aag gaa gag atg gat gaa gct gga aat aaa 641

Ser Lys Ile Asp Thr Leu Lys Glu Glu Met Asp Glu Ala Gly Asn Lys

175

180

185

gta gaa cag tgc aag gat caa ctt gca gca gac atg tac aac ttt atg 689
 Val Glu Gln Cys Lys Asp Gln Leu Ala Ala Asp Met Tyr Asn Phe Met
 190 195 200
 gcc aaa gaa ggg gag tat ggc aaa ttc ttt gtt acg tta tta gaa gcc 737
 Ala Lys Glu Gly Glu Tyr Gly Lys Phe Phe Val Thr Leu Leu Glu Ala
 205 210 215
 caa gca gat tac cat aga aaa gca tta gca gtc tta gaa aag acc ctc 785
 Gln Ala Asp Tyr His Arg Lys Ala Leu Ala Val Leu Glu Lys Thr Leu
 220 225 230
 ccc gaa atg cga gcc cat caa gat aag tgg gcg gaa aaa cca gcc ttt 833
 Pro Glu Met Arg Ala His Gln Asp Lys Trp Ala Glu Lys Pro Ala Phe
 235 240 245 250
 ggg act ccc cta gaa gaa cac ctg aag agg agc ggg cgc gag att gcg 881
 Gly Thr Pro Leu Glu Glu His Leu Lys Arg Ser Gly Arg Glu Ile Ala
 255 260 265
 ctg ccc att gaa gcc tgt gtc atg ctg ctt ctg gag aca gcc atg aag 929
 Leu Pro Ile Glu Ala Cys Val Met Leu Leu Leu Glu Thr Gly Met Lys
 270 275 280
 gag gag ggc ctt ttc cga att ggg gct ggg gcc tcc aag tta aag aag 977
 Glu Glu Gly Leu Phe Arg Ile Gly Ala Gly Ala Ser Lys Leu Lys Lys
 285 290 295
 ctg aaa gct gct ttg gac tgt tct act tct cac ctg gat gag ttc tat 1025
 Leu Lys Ala Ala Leu Asp Cys Ser Thr Ser His Leu Asp Glu Phe Tyr
 300 305 310
 tca gac ccc cat gct gta gca ggt gct tta aaa tcc tat tta cgg gaa 1073
 Ser Asp Pro His Ala Val Ala Gly Ala Leu Lys Ser Tyr Leu Arg Glu

315	320	325	330	
ttg cct gaa cct ttg atg act ttt aat ctg tat gaa gaa tgg aca caa	1121			
Leu Pro Glu Pro Leu Met Thr Phe Asn Leu Tyr Glu Glu Trp Thr Gln				
335	340	345		
gtt gca agt gtg cag gat caa gac aaa aaa ctt caa gac ttg tgg aga	1169			
Val Ala Ser Val Gln Asp Gln Asp Lys Lys Leu Gln Asp Leu Trp Arg				
350	355	360		
aca tgt cag aag ttg cca cca caa aat ttt gtt aac ttt aga tat ttg	1217			
Thr Cys Gln Lys Leu Pro Pro Gln Asn Phe Val Asn Phe Arg Tyr Leu				
365	370	375		
atc aag ttc ctt gca aag ctt gct cag acc agc gat gtg aat aaa atg	1265			
Ile Lys Phe Leu Ala Lys Leu Ala Gln Thr Ser Asp Val Asn Lys Met				
380	385	390		
act ccc agc aac att gcg att glg tia ggc cct aac ttg ita tgg gcc	1313			
Thr Pro Ser Asn Ile Ala Ile Val Leu Gly Pro Asn Leu Leu Trp Ala				
395	400	405	410	
aga aat gaa gga aca ctt gct gaa atg gca gca gcc aca tcc gtc cat	1361			
Arg Asn Glu Gly Thr Leu Ala Glu Met Ala Ala Ala Thr Ser Val His				
415	420	425		
gtg gtt gca gtg att gaa ccc atc att cag cat gcc gac tgg ttc ttc	1409			
Val Val Ala Val Ile Glu Pro Ile Ile Gln His Ala Asp Trp Phe Phe				
430	435	440		
cct gaa gag gtg gaa ttt aat gta tca gaa gca ttt gta cct ctc acc	1457			
Pro Glu Glu Val Glu Phe Asn Val Ser Glu Ala Phe Val Pro Leu Thr				
445	450	455		
acc ccg agt tct aat cac tca ttc cac act gga aac gac tct gac tgg	1505			
Thr Pro Ser Ser Asn His Ser Phe His Thr Gly Asn Asp Ser Asp Ser				

460	465	470	
ggg acc ctg gag agg aag cgg cct gct agc atg gcg gtg atg gaa gga	1553		
Gly Thr Leu Glu Arg Lys Arg Pro Ala Ser Met Ala Val Met Glu Gly			
475	480	485	490
gac ttg gtg aag aag gaa agc ttt ggt gtg aag ctt atg gac ttc cag	1601		
Asp Leu Val Lys Lys Glu Ser Phe Gly Val Lys Leu Met Asp Phe Gln			
495	500	505	
gcc cac cgg cgg ggt ggc act cta aat aga aag cac ata tcc ccc gct	1649		
Ala His Arg Arg Gly Gly Thr Leu Asn Arg Lys His Ile Ser Pro Ala			
510	515	520	
ttc cag ccg cca ctt ccg ccc aca gat ggc agc acc gtg gtg ccc gct	1697		
Phe Gln Pro Pro Leu Pro Pro Thr Asp Gly Ser Thr Val Val Pro Ala			
525	530	535	
ggc cca gag ccc cct ccc cag agc tct agg gct gaa agc agc tct ggg	1745		
Gly Pro Glu Pro Pro Pro Gln Ser Ser Arg Ala Glu Ser Ser Ser Gly			
540	545	550	
ggt ggg act gtc ccc tct tcc gcg ggc ata ctg gag cag ggg ccg agc	1793		
Gly Gly Thr Val Pro Ser Ser Ala Gly Ile Leu Glu Gln Gly Pro Ser			
555	560	565	570
cca ggc gac ggc agt cct ccc aaa ccg aag gac cct gta tct gca gct	1841		
Pro Gly Asp Gly Ser Pro Pro Lys Pro Lys Asp Pro Val Ser Ala Ala			
575	580	585	
gtg cca gca cca ggg aga aac aac agt cag ata gca tct ggc caa aat	1889		
Val Pro Ala Pro Gly Arg Asn Asn Ser Gln Ile Ala Ser Gly Gln Asn			
590	595	600	
cag ccc cag gca gct gct ggc tcc cac cag ctc tcc atg ggc caa cct	1937		

Gln Pro Gln Ala Ala Ala Gly Ser His Gln Leu Ser Met Gly Gln Pro
 605 610 615
 cac aat gct gca ggg ccc agc ccg cat aca ctg cgc cga gct gtt aaa 1985
 His Asn Ala Ala Gly Pro Ser Pro His Thr Leu Arg Arg Ala Val Lys
 620 625 630
 aaa ccc gct cca gca ccc ccg aaa ccg ggc aac cca cct cct ggc cac 2033
 Lys Pro Ala Pro Ala Pro Pro Lys Pro Gly Asn Pro Pro Pro Gly His
 635 640 645 650
 ccc ggg ggc cag agt tct tca gga aca tct cag cat cca ccc agt ctg 2081
 Pro Gly Gly Gln Ser Ser Ser Gly Thr Ser Gln His Pro Pro Ser Leu
 655 660 665
 tca cca aag cca ccc acc cga agc ccc tct cct ccc acc cag cac acg 2129
 Ser Pro Lys Pro Pro Thr Arg Ser Pro Ser Pro Pro Thr Gln His Thr
 670 675 680
 ggc cag cct cca ggc cag ccc tcc gcc ccc tcc cag ctc tca gca ccc 2177
 Gly Gln Pro Pro Gly Gln Pro Ser Ala Pro Ser Gln Leu Ser Ala Pro
 685 690 695
 cgg agg tac tcc agc agc ttg tct cca atc caa gct ccc aat cac cca 2225
 Arg Arg Tyr Ser Ser Ser Leu Ser Pro Ile Gln Ala Pro Asn His Pro
 700 705 710
 ccg ccg cag ccc cct acg cag gcc acg cca ctg atg cac acc aaa ccc 2273
 Pro Pro Gln Pro Pro Thr Gln Ala Thr Pro Leu Met His Thr Lys Pro
 715 720 725 730
 aat agc cag ggc cct ccc aac ccc atg gca ttg ccc agt gag cat gga 2321
 Asn Ser Gln Gly Pro Pro Asn Pro Met Ala Leu Pro Ser Glu His Gly
 735 740 745
 ctt gag cag cca tct cac acc cct ccc cag act cca acg ccc ccc agt 2369

Leu Glu Gln Pro Ser His Thr Pro Pro Gln Thr Pro Thr Pro Pro Ser

750

755

760

act ccg ccc cta gga aaa cag aac ccc agt ctg cca gct cct cag acc 2417

Thr Pro Pro Leu Gly Lys Gln Asn Pro Ser Leu Pro Ala Pro Gln Thr

765

770

775

ctg gca ggg ggt aac cct gaa act gca cag cca cat gct gga acc tta 2465

Leu Ala Gly Gly Asn Pro Glu Thr Ala Gln Pro His Ala Gly Thr Leu

780

785

790

ccg aga ccg aga cca gla cca aag cca agg aac cgg ccc agc gtg ccc 2513

Pro Arg Pro Arg Pro Val Pro Lys Pro Arg Asn Arg Pro Ser Val Pro

795

800

805

810

cca ccc ccc caa cct cct ggt gtc cac tca gct ggg gac agc agc ctc 2561

Pro Pro Pro Gln Pro Pro Gly Val His Ser Ala Gly Asp Ser Ser Leu

815

820

825

acc aac aca gca cca aca gct tcc aag ata gla aca gac tcc aat tcc 2609

Thr Asn Thr Ala Pro Thr Ala Ser Lys Ile Val Thr Asp Ser Asn Ser

830

835

840

agg gtt tca gaa ccg cat cgc agc atc ttt cct gaa atg cac tca gac 2657

Arg Val Ser Glu Pro His Arg Ser Ile Phe Pro Glu Met His Ser Asp

845

850

855

tca gcc agc aaa gac gtg cct ggc cgc atc ctg ctg gat ata gac aat 2705

Ser Ala Ser Lys Asp Val Pro Gly Arg Ile Leu Leu Asp Ile Asp Asn

860

865

870

gat acc gag agc act gcc ctg tgaagaaagc cctttcccag cccctccacca 2756

Asp Thr Glu Ser Thr Ala Leu

875

880

cttccaccct ggcgagtgga gcaggggcag gcgaacctct ttccttgag accgaacagt 2816
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 gtactgttct tttttttttt tttaaacaat gtaattgcta cttgataagg accgaacatt 3416
 attctagttt catgtttaat ttgaattaaa tatattctgt ggtttatatg 3466

<210> 146

<211> 881

<212> PRT

<213> Homo sapiens

<400> 146

Met Lys Lys Gln Phe Asn Arg Met Lys Gln Leu Ala Asn Gln Thr Val

1

5

10

15

Gly Arg Ala Glu Lys Thr Glu Val Leu Ser Glu Asp Leu Leu Gln Ile

20

25

30

Glu Arg Arg Leu Asp Thr Val Arg Ser Ile Cys His His Ser His Lys

35

40

45

Arg Leu Val Ala Cys Phe Gln Gly Gln His Gly Thr Asp Ala Glu Arg

50

55

60

Arg His Lys Lys Leu Pro Leu Thr Ala Leu Ala Gln Asn Met Gln Glu

65	70	75	80
Ala Ser Thr Gln Leu Glu Asp Ser Leu Leu Gly Lys Met Leu Glu Thr			
85	90	95	
Cys Gly Asp Ala Glu Asn Gln Leu Ala Leu Glu Leu Ser Gln His Glu			
100	105	110	
Val Phe Val Glu Lys Glu Ile Val Asp Pro Leu Tyr Gly Ile Ala Glu			
115	120	125	
Val Glu Ile Pro Asn Ile Gln Lys Gln Arg Lys Gln Leu Ala Arg Leu			
130	135	140	
Val Leu Asp Trp Asp Ser Val Arg Ala Arg Trp Asn Gln Ala His Lys			
145	150	155	160
Ser Ser Gly Thr Asn Phe Gln Gly Leu Pro Ser Lys Ile Asp Thr Leu			
165	170	175	
Lys Glu Glu Met Asp Glu Ala Gly Asn Lys Val Glu Gln Cys Lys Asp			
180	185	190	
Gln Leu Ala Ala Asp Met Tyr Asn Phe Met Ala Lys Glu Gly Glu Tyr			
195	200	205	
Gly Lys Phe Phe Val Thr Leu Leu Glu Ala Gln Ala Asp Tyr His Arg			
210	215	220	
Lys Ala Leu Ala Val Leu Glu Lys Thr Leu Pro Glu Met Arg Ala His			
225	230	235	240
Gln Asp Lys Trp Ala Glu Lys Pro Ala Phe Gly Thr Pro Leu Glu Glu			
245	250	255	
His Leu Lys Arg Ser Gly Arg Glu Ile Ala Leu Pro Ile Glu Ala Cys			
260	265	270	
Val Met Leu Leu Leu Glu Thr Gly Met Lys Glu Glu Gly Leu Phe Arg			
275	280	285	

Ile Gly Ala Gly Ala Ser Lys Leu Lys Lys Leu Lys Ala Ala Leu Asp
 290 295 300
 Cys Ser Thr Ser His Leu Asp Glu Phe Tyr Ser Asp Pro His Ala Val
 305 310 315 320
 Ala Gly Ala Leu Lys Ser Tyr Leu Arg Glu Leu Pro Glu Pro Leu Met
 325 330 335
 Thr Phe Asn Leu Tyr Glu Glu Trp Thr Gln Val Ala Ser Val Gln Asp
 340 345 350
 Gln Asp Lys Lys Leu Gln Asp Leu Trp Arg Thr Cys Gln Lys Leu Pro
 355 360 365
 Pro Gln Asn Phe Val Asn Phe Arg Tyr Leu Ile Lys Phe Leu Ala Lys
 370 375 380
 Leu Ala Gln Thr Ser Asp Val Asn Lys Met Thr Pro Ser Asn Ile Ala
 385 390 395 400
 Ile Val Leu Gly Pro Asn Leu Leu Trp Ala Arg Asn Glu Gly Thr Leu
 405 410 415
 Ala Glu Met Ala Ala Ala Thr Ser Val His Val Val Ala Val Ile Glu
 420 425 430
 Pro Ile Ile Gln His Ala Asp Trp Phe Phe Pro Glu Glu Val Glu Phe
 435 440 445
 Asn Val Ser Glu Ala Phe Val Pro Leu Thr Thr Pro Ser Ser Asn His
 450 455 460
 Ser Phe His Thr Gly Asn Asp Ser Asp Ser Gly Thr Leu Glu Arg Lys
 465 470 475 480
 Arg Pro Ala Ser Met Ala Val Met Glu Gly Asp Leu Val Lys Lys Glu
 485 490 495

Ser Phe Gly Val Lys Leu Met Asp Phe Gln Ala His Arg Arg Gly Gly

500

505

510

Thr Leu Asn Arg Lys His Ile Ser Pro Ala Phe Gln Pro Pro Leu Pro

515

520

525

Pro Thr Asp Gly Ser Thr Val Val Pro Ala Gly Pro Glu Pro Pro Pro

530

535

540

Gln Ser Ser Arg Ala Glu Ser Ser Ser Gly Gly Gly Thr Val Pro Ser

545

550

555

560

Ser Ala Gly Ile Leu Glu Gln Gly Pro Ser Pro Gly Asp Gly Ser Pro

565

570

575

Pro Lys Pro Lys Asp Pro Val Ser Ala Ala Val Pro Ala Pro Gly Arg

580

585

590

Asn Asn Ser Gln Ile Ala Ser Gly Gln Asn Gln Pro Gln Ala Ala Ala

595

600

605

Gly Ser His Gln Leu Ser Met Gly Gln Pro His Asn Ala Ala Gly Pro

610

615

620

Ser Pro His Thr Leu Arg Arg Ala Val Lys Lys Pro Ala Pro Ala Pro

625

630

635

640

Pro Lys Pro Gly Asn Pro Pro Pro Gly His Pro Gly Gly Gln Ser Ser

645

650

655

Ser Gly Thr Ser Gln His Pro Pro Ser Leu Ser Pro Lys Pro Pro Thr

660

665

670

Arg Ser Pro Ser Pro Pro Thr Gln His Thr Gly Gln Pro Pro Gly Gln

675

680

685

Pro Ser Ala Pro Ser Gln Leu Ser Ala Pro Arg Arg Tyr Ser Ser Ser

690

695

700

Leu Ser Pro Ile Gln Ala Pro Asn His Pro Pro Pro Gln Pro Pro Thr

705 710 715 720
 Gln Ala Thr Pro Leu Met His Thr Lys Pro Asn Ser Gln Gly Pro Pro
 725 730 735
 Asn Pro Met Ala Leu Pro Ser Glu His Gly Leu Glu Gln Pro Ser His
 740 745 750
 Thr Pro Pro Gln Thr Pro Thr Pro Pro Ser Thr Pro Pro Leu Gly Lys
 755 760 765
 Gln Asn Pro Ser Leu Pro Ala Pro Gln Thr Leu Ala Gly Gly Asn Pro
 770 775 780
 Glu Thr Ala Gln Pro His Ala Gly Thr Leu Pro Arg Pro Arg Pro Val
 785 790 795 800
 Pro Lys Pro Arg Asn Arg Pro Ser Val Pro Pro Pro Pro Gln Pro Pro
 805 810 815
 Gly Val His Ser Ala Gly Asp Ser Ser Leu Thr Asn Thr Ala Pro Thr
 820 825 830
 Ala Ser Lys Ile Val Thr Asp Ser Asn Ser Arg Val Ser Glu Pro His
 835 840 845
 Arg Ser Ile Phe Pro Glu Met His Ser Asp Ser Ala Ser Lys Asp Val
 850 855 860
 Pro Gly Arg Ile Leu Leu Asp Ile Asp Asn Asp Thr Glu Ser Thr Ala
 865 870 875 880
 Leu

<210> 147

<211> 3021

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (140).. (1105)

<400> 147

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 acagccctgtt ccaagtgtgg cttaatccgt ctccaccacc agatctttct ccgtggattc 120
 ctctgctaag accgctgcc atg cca gtc acg gta acc cgc acc acc atc aca 172

Met Pro Val Thr Val Thr Arg Thr Thr Ile Thr

1

5

10

acc acc acg acg tca tct tcg ggc ctg ggg tcc ccc atg atc gtc ggg 220

Thr Thr Thr Thr Ser Ser Ser Gly Leu Gly Ser Pro Met Ile Val Gly

15

20

25

tcc cct cgg gcc ctg aca cag ccc ctg ggt ctc ctt cgc ctg ctg cag 268

Ser Pro Arg Ala Leu Thr Gln Pro Leu Gly Leu Leu Arg Leu Leu Gln

30

35

40

ctg gtc tct acc tgc gtc gcc ttc tcg ctg gtc gct agc gtc ggc gcc 316

Leu Val Ser Thr Cys Val Ala Phe Ser Leu Val Ala Ser Val Gly Ala

45

50

55

tgg acg ggg tcc atg ggc aac tgg tcc atg ttc acc tgg tgc ttc tgc 364

Trp Thr Gly Ser Met Gly Asn Trp Ser Met Phe Thr Trp Cys Phe Cys

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65

70

75

ttc tcc gtc acc ctg atc atc ctc atc gtc gag ctg tgc ggg ctc cag 412

Phe Ser Val Thr Leu Ile Ile Leu Ile Val Glu Leu Cys Gly Leu Gln

80

85

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Ala Arg Phe Pro Leu Ser Trp Arg Asn Phe Pro Ile Thr Phe Ala Cys

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Tyr Ala Gly Leu Phe Cys Leu Ser Ala Ser Ile Ile Tyr Pro Thr Thr			
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Tyr Val Gln Phe Leu Ser His Gly Arg Ser Arg Asp His Ala Ile Ala			
125	130	135	
gcc acc ttc ttc tcc tgc atc gcg tgt gtg gct tac gcc acc gaa gtg			604
Ala Thr Phe Phe Ser Cys Ile Ala Cys Val Ala Tyr Ala Thr Glu Val			
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gcc tgg acc cgg gcc cgg ccc ggc gag atc act ggc tat atg gcc acc			652
Ala Trp Thr Arg Ala Arg Pro Gly Glu Ile Thr Gly Tyr Met Ala Thr			
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Val Pro Gly Leu Leu Lys Val Leu Glu Thr Phe Val Ala Cys Ile Ile			
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Phe Ala Phe Ile Ser Asp Pro Asn Leu Tyr Gln His Gln Pro Ala Leu			
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gag tgg tgc gtg gcg gtg tac gcc atc tgc ttc atc cta gcg gcc atc			796
Glu Trp Cys Val Ala Val Tyr Ala Ile Cys Phe Ile Leu Ala Ala Ile			
205	210	215	
gcc atc ctg ctg aac ctg ggg gag tgc acc aac gtg cta ccc atc ccc			844
Ala Ile Leu Leu Asn Leu Gly Glu Cys Thr Asn Val Leu Pro Ile Pro			
220	225	230	235
ttc ccc agc ttc ctg tcg ggg ctg gcc ttg ctg tct gtc ctc ctc tat			892
Phe Pro Ser Phe Leu Ser Gly Leu Ala Leu Leu Ser Val Leu Leu Tyr			

240 245 250
 gcc acc gcc ctt gtt ctc tgg ccc ctc tac cag ttc gat gag aag tat 940
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 ggc ggc cag cct cgg cgc tgc aga gat gta agc tgc agc cgc agc cat 988
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 gcc tac tac gtg tgt gcc tgg gac cgc cga ctg gct gtg gcc atc ctg 1036
 Ala Tyr Tyr Val Cys Ala Trp Asp Arg Arg Leu Ala Val Ala Ile Leu
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 acg gcc atc aac cta ctg gcg tat gtg gct gac ctg gtg cac tct gcc 1084
 Thr Ala Ile Asn Leu Leu Ala Tyr Val Ala Asp Leu Val His Ser Ala
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<212> PRT

<213> Homo sapiens

<400> 148

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 Thr Gln Pro Leu Gly Leu Leu Arg Leu Leu Gln Leu Val Ser Thr Cys
 35 40 45
 Val Ala Phe Ser Leu Val Ala Ser Val Gly Ala Trp Thr Gly Ser Met
 50 55 60
 Gly Asn Trp Ser Met Phe Thr Trp Cys Phe Cys Phe Ser Val Thr Leu
 65 70 75 80
 Ile Ile Leu Ile Val Glu Leu Cys Gly Leu Gln Ala Arg Phe Pro Leu
 85 90 95
 Ser Trp Arg Asn Phe Pro Ile Thr Phe Ala Cys Tyr Ala Gly Leu Phe
 100 105 110
 Cys Leu Ser Ala Ser Ile Ile Tyr Pro Thr Thr Tyr Val Gln Phe Leu
 115 120 125
 Ser His Gly Arg Ser Arg Asp His Ala Ile Ala Ala Thr Phe Phe Ser
 130 135 140
 Cys Ile Ala Cys Val Ala Tyr Ala Thr Glu Val Ala Trp Thr Arg Ala
 145 150 155 160
 Arg Pro Gly Glu Ile Thr Gly Tyr Met Ala Thr Val Pro Gly Leu Leu
 165 170 175
 Lys Val Leu Glu Thr Phe Val Ala Cys Ile Ile Phe Ala Phe Ile Ser
 180 185 190
 Asp Pro Asn Leu Tyr Gln His Gln Pro Ala Leu Glu Trp Cys Val Ala
 195 200 205

Val Tyr Ala Ile Cys Phe Ile Leu Ala Ala Ile Ala Ile Leu Leu Asn

210

215

220

Leu Gly Glu Cys Thr Asn Val Leu Pro Ile Pro Phe Pro Ser Phe Leu

225

230

235

240

Ser Gly Leu Ala Leu Leu Ser Val Leu Leu Tyr Ala Thr Ala Leu Val

245

250

255

Leu Trp Pro Leu Tyr Gln Phe Asp Glu Lys Tyr Gly Gly Gln Pro Arg

260

265

270

Arg Ser Arg Asp Val Ser Cys Ser Arg Ser His Ala Tyr Tyr Val Cys

275

280

285

Ala Trp Asp Arg Arg Leu Ala Val Ala Ile Leu Thr Ala Ile Asn Leu

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Leu Ala Tyr Val Ala Asp Leu Val His Ser Ala His Leu Val Phe Val

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Lys Val

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 Ser Gln Gly Val Val Leu Thr Ala Tyr His Pro Ser Gly Lys Asp Gln
 10 15 20
 gcc gtc ggg aac agc cat gca aag gca ggg gag gaa gcc acc tcg agt 152
 Ala Val Gly Asn Ser His Ala Lys Ala Gly Glu Glu Ala Thr Ser Ser
 25 30 35
 cgc aga tat ggc cag tac act atg aac cag gaa agc acc acc atc aaa 200
 Arg Arg Tyr Gly Gln Tyr Thr Met Asn Gln Glu Ser Thr Thr Ile Lys
 40 45 50
 gtt atg gag aag cct cca ttt gat cga tca att tcc cag gat tct ttg 248
 Val Met Glu Lys Pro Pro Phe Asp Arg Ser Ile Ser Gln Asp Ser Leu
 55 60 65 70
 gat gaa cta tct atg gaa gac tal tgg ata gaa cta gaa aac atc aag 296
 Asp Glu Leu Ser Met Glu Asp Tyr Trp Ile Glu Leu Glu Asn Ile Lys
 75 80 85
 aaa tct agt gaa aac agc caa gaa gat caa gag gtg gtt gtt gtc aaa 344
 Lys Ser Ser Glu Asn Ser Gln Glu Asp Gln Glu Val Val Val Val Lys
 90 95 100
 gag cct gat gag gga gaa ttg gaa gaa gag tgg ctt aaa gag gcc ggt 392
 Glu Pro Asp Glu Gly Glu Leu Glu Glu Glu Trp Leu Lys Glu Ala Gly
 105 110 115
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 Leu Ser Asn Leu Phe Gly Glu Ser Ala Gly Asp Pro Gln Glu Ser Ile
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 gtg ttt tta tca aca ttg acg cgg acc cag gca gca gca gtt cag aag 488
 Val Phe Leu Ser Thr Leu Thr Arg Thr Gln Ala Ala Ala Val Gln Lys

135	140	145	150	
cga gta gag acg gtc tcc cag acc ttg agg aaa aaa aac aaa cag tac	536			
Arg Val Glu Thr Val Ser Gln Thr Leu Arg Lys Lys Asn Lys Gln Tyr				
155	160	165		
cag att cct gac gtc aga gac ata ttt gct caa cag aga gaa tca aaa	584			
Gln Ile Pro Asp Val Arg Asp Ile Phe Ala Gln Gln Arg Glu Ser Lys				
170	175	180		
gaa aca gct cca ggt ggc act gaa tcg cag tca ctt aga aca aat gaa	632			
Glu Thr Ala Pro Gly Gly Thr Glu Ser Gln Ser Leu Arg Thr Asn Glu				
185	190	195		
aac aaa tac caa gga aga gat gac gag gca tct aac ctt gtt ggt gaa	680			
Asn Lys Tyr Gln Gly Arg Asp Asp Glu Ala Ser Asn Leu Val Gly Glu				
200	205	210		
gag aag ctg atc cca cct gag gag acg cct gcc cct gaa aca gac atc	728			
Glu Lys Leu Ile Pro Pro Glu Glu Thr Pro Ala Pro Glu Thr Asp Ile				
215	220	225	230	
aac ctg gag gta tca ttt gcc gag caa gca ctc aat cag aaa gag agc	776			
Asn Leu Glu Val Ser Phe Ala Glu Gln Ala Leu Asn Gln Lys Glu Ser				
235	240	245		
tcc aag gag aaa atc cag aag agc aaa ggc gat gat gcc aca tta cct	824			
Ser Lys Glu Lys Ile Gln Lys Ser Lys Gly Asp Asp Ala Thr Leu Pro				
250	255	260		
agt ttc aga ttg cca aaa gac aaa acg ggt acc aca agg att ggt gac	872			
Ser Phe Arg Leu Pro Lys Asp Lys Thr Gly Thr Thr Arg Ile Gly Asp				
265	270	275		
ctc gca ccc cag gac atg aag aaa gtt tgc cat tta gcc cta att gag	920			
Leu Ala Pro Gln Asp Met Lys Lys Val Cys His Leu Ala Leu Ile Glu				

280	285	290	
ctg act gcc ctc tat gat gta ttg ggt att gag ctg aaa caa caa aaa	968		
Leu Thr Ala Leu Tyr Asp Val Leu Gly Ile Glu Leu Lys Gln Gln Lys			
295	300	305	310
gct glg aaa atc aaa aca aaa gat tct ggt ctt ttt tgc gtt cca ttg	1016		
Ala Val Lys Ile Lys Thr Lys Asp Ser Gly Leu Phe Cys Val Pro Leu			
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aca gcg cta tta gaa caa gat cag agg aaa gta cca gga atg cga ata	1064		
Thr Ala Leu Leu Glu Gln Asp Gln Arg Lys Val Pro Gly Met Arg Ile			
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ccc ttg atc ttt caa aaa ctg att tct cga att gaa gag aga ggt ttg	1112		
Pro Leu Ile Phe Gln Lys Leu Ile Ser Arg Ile Glu Glu Arg Gly Leu			
345	350	355	
gaa aca gaa ggc ctc tta cgg atc cct gga gct gcc att aga atc aag	1160		
Glu Thr Glu Gly Leu Leu Arg Ile Pro Gly Ala Ala Ile Arg Ile Lys			
360	365	370	
aat ctt tgc caa gaa cta gaa gca aag ttt tat gaa ggg act ttt aat	1208		
Asn Leu Cys Gln Glu Leu Glu Ala Lys Phe Tyr Glu Gly Thr Phe Asn			
375	380	385	390
tgg gaa agt gtc aaa cag cat gat gcc gcc agc ctg ctg aag ctc ttc	1256		
Trp Glu Ser Val Lys Gln His Asp Ala Ala Ser Leu Leu Lys Leu Phe			
395	400	405	
att cgg gag ttg ccc cag cca ctg ctc agt gtg gag tat ctc aaa gcc	1304		
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ttt cag gct gtc cag aat ctt cca acc aag aag cag caa cta cag gct	1352		

Phe Gln Ala Val Gln Asn Leu Pro Thr Lys Lys Gln Gln Leu Gln Ala

425

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440

445

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455

460

465

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Asn Lys Met Thr Val Met Asn Val Ala Met Val Met Ala Pro Asn Leu

475

480

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Phe Met Cys His Ala Leu Gly Leu Lys Ser Ser Glu Gln Arg Glu Phe

490

495

500

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Val Met Ala Ala Gly Thr Ala Asn Thr Met His Leu Leu Ile Lys Tyr

505

510

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caa aaa ctt ctg tgg aca att ccc aag ttt att gta aac caa gtg agg 1640

Gln Lys Leu Leu Trp Thr Ile Pro Lys Phe Ile Val Asn Gln Val Arg

520

525

530

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Lys Gln Asn Thr Glu Asn His Lys Lys Asp Lys Arg Ala Met Lys Lys

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Leu Leu Lys Lys Met Ala Tyr Asp Arg Glu Lys Tyr Glu Lys Gln Asp

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<212> PRT

<213> Homo sapiens

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Glu Glu Ala Thr Ser Ser Arg Arg Tyr Gly Gln Tyr Thr Met Asn Gln

35 40 45

Glu Ser Thr Thr Ile Lys Val Met Glu Lys Pro Pro Phe Asp Arg Ser

50 55 60

Ile Ser Gln Asp Ser Leu Asp Glu Leu Ser Met Glu Asp Tyr Trp Ile

65 70 75 80

Glu Leu Glu Asn Ile Lys Lys Ser Ser Glu Asn Ser Gln Glu Asp Gln

85 90 95

Glu Val Val Val Val Lys Glu Pro Asp Glu Gly Glu Leu Glu Glu Glu

100 105 110

Trp Leu Lys Glu Ala Gly Leu Ser Asn Leu Phe Gly Glu Ser Ala Gly

115 120 125

Asp Pro Gln Glu Ser Ile Val Phe Leu Ser Thr Leu Thr Arg Thr Gln
 130 135 140
 Ala Ala Ala Val Gln Lys Arg Val Glu Thr Val Ser Gln Thr Leu Arg
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 Lys Lys Asn Lys Gln Tyr Gln Ile Pro Asp Val Arg Asp Ile Phe Ala
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 Ser Leu Arg Thr Asn Glu Asn Lys Tyr Gln Gly Arg Asp Asp Glu Ala
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 Ser Asn Leu Val Gly Glu Glu Lys Leu Ile Pro Pro Glu Glu Thr Pro
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 Ala Pro Glu Thr Asp Ile Asn Leu Glu Val Ser Phe Ala Glu Gln Ala
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 260 265 270
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 275 280 285
 His Leu Ala Leu Ile Glu Leu Thr Ala Leu Tyr Asp Val Leu Gly Ile
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 325 330 335

Val Pro Gly Met Arg Ile Pro Leu Ile Phe Gln Lys Leu Ile Ser Arg
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Ile Glu Glu Arg Gly Leu Glu Thr Glu Gly Leu Leu Arg Ile Pro Gly
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Val Glu Tyr Leu Lys Ala Phe Gln Ala Val Gln Asn Leu Pro Thr Lys
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Lys Gln Gln Leu Gln Ala Leu Asn Leu Leu Gly Ile Leu Leu Pro Asp
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465 470 475 480
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485 490 495
Ser Glu Gln Arg Glu Phe Val Met Ala Ala Gly Thr Ala Asn Thr Met
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His Leu Leu Ile Lys Tyr Gln Lys Leu Leu Trp Thr Ile Pro Lys Phe
515 520 525
Ile Val Asn Gln Val Arg Lys Gln Asn Thr Glu Asn His Lys Lys Asp
530 535 540
Lys Arg Ala Met Lys Lys Leu Leu Lys Lys Met Ala Tyr Asp Arg Glu

545 550 555 560
 Lys Tyr Glu Lys Gln Asp Lys Ser Thr Asn Asp Ala Asp Val Pro Gln
 565 570 575
 Gly Val Ile Arg Val Gln Ala Pro His Leu Ser Lys Val Ser Met Ala
 580 585 590
 Ile Gln Leu Thr Glu Glu Leu Lys Ala Ser Asp Val Leu Ala Arg Phe
 595 600 605
 Leu Ser Gln Glu Ser Gly Val Ala Gln Thr Leu Lys Lys Gly Glu Val
 610 615 620
 Phe Leu Tyr Glu Ile Gly Gly Asn Ile Gly Glu Arg Cys Leu Asp Asp
 625 630 635 640
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 Val Ile Lys Ser Lys Pro Leu
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 Asn Ser Thr Leu Ser Asp Ser Gly Met Ile Asp Asn Leu Pro Asp Ser
 20 25 30
 cca gac gag gta gcc aag gag ctg gag ctg ctc ggg gga tgg aca gat 143
 Pro Asp Glu Val Ala Lys Glu Leu Glu Leu Leu Gly Gly Trp Thr Asp
 35 40 45
 gac aaa aaa gta cca ggc aga atg tac agt aat aac cct ttc tgg aat 191
 Asp Lys Lys Val Pro Gly Arg Met Tyr Ser Asn Asn Pro Phe Trp Asn
 50 55 60
 ggg gtc cag acc aat cca ttt ctg aat ggg aac gtg ccc gtc atg ccc 239
 Gly Val Gln Thr Asn Pro Phe Leu Asn Gly Asn Val Pro Val Met Pro
 65 70 75
 agc ctg gat gag ctg aat ccc aaa agt act gtg gat ttg ctc ctt ttt 287
 Ser Leu Asp Glu Leu Asn Pro Lys Ser Thr Val Asp Leu Leu Leu Phe
 80 85 90 95
 gac gca ggt aca tcc tcc ttc acc gaa tcc agc tca gcc acc acg aat 335
 Asp Ala Gly Thr Ser Ser Phe Thr Glu Ser Ser Ser Ala Thr Thr Asn
 100 105 110
 agc act ggc aac atc ttc gat gag ctt cca gtc aca aac ggg ctc cac 383
 Ser Thr Gly Asn Ile Phe Asp Glu Leu Pro Val Thr Asn Gly Leu His
 115 120 125
 gca gag ccg ccg gtc agg cgg gac aac ccc ttc ttc aga agc aag cgc 431
 Ala Glu Pro Pro Val Arg Arg Asp Asn Pro Phe Phe Arg Ser Lys Arg
 130 135 140
 tcc tac agt ctc tcg gaa ctc tcc gtc ctc caa gcc aag tcc gac gct 479
 Ser Tyr Ser Leu Ser Glu Leu Ser Val Leu Gln Ala Lys Ser Asp Ala

145	150	155	
ccc aca tcg tcg agt ttc ttc acc ggc ttg aaa tca cct gcc ccc gag	527		
Pro Thr Ser Ser Ser Phe Phe Thr Gly Leu Lys Ser Pro Ala Pro Glu			
160	165	170	175
caa ttt cag agc cgg gag gat ttt cga act gcc tgg cta aac cac agg	575		
Gln Phe Gln Ser Arg Glu Asp Phe Arg Thr Ala Trp Leu Asn His Arg			
180	185	190	
aag ctg gcc cgg tct tgc cac gac ctg gac ttg ctt ggc caa agc cct	623		
Lys Leu Ala Arg Ser Cys His Asp Leu Asp Leu Leu Gly Gln Ser Pro			
195	200	205	
ggt tgg ggc cag acc caa gcc gtg gag aca aac atc gtg tgc aag ctg	671		
Gly Trp Gly Gln Thr Gln Ala Val Glu Thr Asn Ile Val Cys Lys Leu			
210	215	220	
gat agc tcc ggg ggt gct gtc cag ctt cct gac acc agc atc agc atc	719		
Asp Ser Ser Gly Gly Ala Val Gln Leu Pro Asp Thr Ser Ile Ser Ile			
225	230	235	
cac gtg ccc gag ggc cac gtc gcc cct ggg gag acc cag cag atc tcc	767		
His Val Pro Glu Gly His Val Ala Pro Gly Glu Thr Gln Gln Ile Ser			
240	245	250	255
atg aaa gcc ctg ctg gac ccc ccg ctg gag ctc aac agt gac agg tcc	815		
Met Lys Ala Leu Leu Asp Pro Pro Leu Glu Leu Asn Ser Asp Arg Ser			
260	265	270	
tgc agc atc agc cct gtg ctg gag gtc aag ctg agc aac ctg gag gtg	863		
Cys Ser Ile Ser Pro Val Leu Glu Val Lys Leu Ser Asn Leu Glu Val			
275	280	285	
aaa acc tct atc atc ttg gag atg aaa gtg tca gcc gag ata aaa aat	911		
Lys Thr Ser Ile Ile Leu Glu Met Lys Val Ser Ala Glu Ile Lys Asn			

290	295	300	
gac ctt ttt agc aaa agc aca gtg ggc ctc cag tgc ctg agg agc gac			959
Asp Leu Phe Ser Lys Ser Thr Val Gly Leu Gln Cys Leu Arg Ser Asp			
305	310	315	
tcg aag gaa ggg cca tat gtc tcc gtc ccg ctc aac tgc agc tgt ggg			1007
Ser Lys Glu Gly Pro Tyr Val Ser Val Pro Leu Asn Cys Ser Cys Gly			
320	325	330	335
gac acg gtc cag gca cag ctg cac aac ctg gag ccc tgt atg tac gtg			1055
Asp Thr Val Gln Ala Gln Leu His Asn Leu Glu Pro Cys Met Tyr Val			
340	345	350	
gct gtc gtg gcc cat ggc cca agc atc ctc tac cct tcc acc gtg tgg			1103
Ala Val Val Ala His Gly Pro Ser Ile Leu Tyr Pro Ser Thr Val Trp			
355	360	365	
gac ttc atc aat aaa aaa gtc aca gtg ggt ctc tac ggc cct aaa cac			1151
Asp Phe Ile Asn Lys Lys Val Thr Val Gly Leu Tyr Gly Pro Lys His			
370	375	380	
atc cac cca tcc ttc aag acg gta gtg acc att ttt ggg cat gac tgt			1199
Ile His Pro Ser Phe Lys Thr Val Val Thr Ile Phe Gly His Asp Cys			
385	390	395	
gcc cca aag acg ctc ctg gtc agc gag gtc aca cgc cag gca ccc aac			1247
Ala Pro Lys Thr Leu Leu Val Ser Glu Val Thr Arg Gln Ala Pro Asn			
400	405	410	415
cct gcc ccg gtg gcc ctg cag ctg tgg ggg aag cac cag ttc gtt ttt			1295
Pro Ala Pro Val Ala Leu Gln Leu Trp Gly Lys His Gln Phe Val Leu			
420	425	430	
tcc agg ccc cag gat ctc aag gtc tgt atg ttt tcc aat atg acg aat			1343

Ser Arg Pro Gln Asp Leu Lys Val Cys Met Phe Ser Asn Met Thr Asn

435

440

445

tac gag gtc aaa gcc agc gag cag gcc aaa glg gtg cga gga ttc cag 1391

Tyr Glu Val Lys Ala Ser Glu Gln Ala Lys Val Val Arg Gly Phe Gln

450

455

460

ctg aag ctg ggc aag gtg agc cgc ctg atc ttc ccc atc acc tcc cag 1439

Leu Lys Leu Gly Lys Val Ser Arg Leu Ile Phe Pro Ile Thr Ser Gln

465

470

475

aac ccc aac gag ctc tct gac ttc acg ctg cgg gtt cag gtg aag gac 1487

Asn Pro Asn Glu Leu Ser Asp Phe Thr Leu Arg Val Gln Val Lys Asp

480

485

490

495

gac cag gag gcc atc ctc acc cag ttt tgt gtc cag act cct cag cca 1535

Asp Gln Glu Ala Ile Leu Thr Gln Phe Cys Val Gln Thr Pro Gln Pro

500

505

510

ccc cct aaa agt gcc atc aag cct tcc ggg caa agg agg ttt ctc aag 1583

Pro Pro Lys Ser Ala Ile Lys Pro Ser Gly Gln Arg Arg Phe Leu Lys

515

520

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aag aac gaa gtc ggg aaa atc atc ctg tcc ccg ttt gcc acc act aca 1631

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530

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aag tac ccg act ttc cag gac cgc ccg gtg tcc agc ctc aag ttt ggt 1679

Lys Tyr Pro Thr Phe Gln Asp Arg Pro Val Ser Ser Leu Lys Phe Gly

545

550

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aag ttg ctc aag act gtg gtg cgg cag aac aag aac cac tac ctg ctg 1727

Lys Leu Leu Lys Thr Val Val Arg Gln Asn Lys Asn His Tyr Leu Leu

560

565

570

575

gag tac aag aag ggc gac ggg atc gcc ctg ctc agc gag gag cgg gtc 1775

Glu Tyr Lys Lys Gly Asp Gly Ile Ala Leu Leu Ser Glu Glu Arg Val
 580 585 590
 agg ctc cgg ggc cag ctg tgg acc aag gag tgg tac atc ggc tac tac 1823
 Arg Leu Arg Gly Gln Leu Trp Thr Lys Glu Trp Tyr Ile Gly Tyr Tyr
 595 600 605
 cag ggc agg gtg ggc ctc gtg cac acc aag aac gtg ctg gtg gtc ggc 1871
 Gln Gly Arg Val Gly Leu Val His Thr Lys Asn Val Leu Val Val Gly
 610 615 620
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 Arg Ala Arg Pro Ser Leu Cys Ser Gly Pro Glu Leu Ser Thr Ser Val
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 640 645 650 655
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 Ala Ser Val Arg Thr Leu Leu Met Glu Asn Ile Ser Ser Trp Arg Ser
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 675 680 685
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 Arg Ala Glu Leu Asp Ser Glu Pro Glu Arg Val Ala Ser Val Leu Glu
 690 695 700
 aag ctg aag gag gac tgt aac aac act gag aac aaa gaa cgg aag tcc 2159
 Lys Leu Lys Glu Asp Cys Asn Asn Thr Glu Asn Lys Glu Arg Lys Ser
 705 710 715

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ctg gtg gtc aga ctc atc cag gac ttt gtg ctc ctg acc acg gct gla	2255
Leu Val Val Arg Leu Ile Gln Asp Phe Val Leu Leu Thr Thr Ala Val	
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Gly Val Val Asp Ser Glu Ala Met Trp Lys Pro Ala Tyr Asp Phe Leu	
785 790 795	
ctc acc tgg agc cat cag atc ggg gac agc tac cgg gat gtc atc cag	2447
Leu Thr Trp Ser His Gln Ile Gly Asp Ser Tyr Arg Asp Val Ile Gln	
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gag ctg cac ctg ggc ctg gac aag atg aaa aac ccc atc acc aag cgc	2495
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tgg aag cac ctc act ggg act ctg atc ttg gtg aac tcc ctg gac gtt	2543
Trp Lys His Leu Thr Gly Thr Leu Ile Leu Val Asn Ser Leu Asp Val	
835 840 845	
ctg aga gca gcc gcc ttc agc cct gcg gac cag gac gac ttc gtg att	2591
Leu Arg Ala Ala Ala Phe Ser Pro Ala Asp Gln Asp Asp Phe Val Ile	
850 855 860	

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<211> 863

<212> PRT

<213> Homo sapiens

<400> 152

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Asp Glu Val Ala Lys Glu Leu Glu Leu Leu Gly Gly Trp Thr Asp Asp

35 40 45

Lys Lys Val Pro Gly Arg Met Tyr Ser Asn Asn Pro Phe Trp Asn Gly

50 55 60

Val Gln Thr Asn Pro Phe Leu Asn Gly Asn Val Pro Val Met Pro Ser

65 70 75 80

Leu Asp Glu Leu Asn Pro Lys Ser Thr Val Asp Leu Leu Leu Phe Asp

85 90 95

Ala Gly Thr Ser Ser Phe Thr Glu Ser Ser Ser Ala Thr Thr Asn Ser

100 105 110

Thr Gly Asn Ile Phe Asp Glu Leu Pro Val Thr Asn Gly Leu His Ala

115	120	125	
Glu Pro Pro Val Arg Arg Asp Asn Pro Phe Phe Arg Ser Lys Arg Ser			
130	135	140	
Tyr Ser Leu Ser Glu Leu Ser Val Leu Gln Ala Lys Ser Asp Ala Pro			
145	150	155	160
Thr Ser Ser Ser Phe Phe Thr Gly Leu Lys Ser Pro Ala Pro Glu Gln			
165	170	175	
Phe Gln Ser Arg Glu Asp Phe Arg Thr Ala Trp Leu Asn His Arg Lys			
180	185	190	
Leu Ala Arg Ser Cys His Asp Leu Asp Leu Leu Gly Gln Ser Pro Gly			
195	200	205	
Trp Gly Gln Thr Gln Ala Val Glu Thr Asn Ile Val Cys Lys Leu Asp			
210	215	220	
Ser Ser Gly Gly Ala Val Gln Leu Pro Asp Thr Ser Ile Ser Ile His			
225	230	235	240
Val Pro Glu Gly His Val Ala Pro Gly Glu Thr Gln Gln Ile Ser Met			
245	250	255	
Lys Ala Leu Leu Asp Pro Pro Leu Glu Leu Asn Ser Asp Arg Ser Cys			
260	265	270	
Ser Ile Ser Pro Val Leu Glu Val Lys Leu Ser Asn Leu Glu Val Lys			
275	280	285	
Thr Ser Ile Ile Leu Glu Met Lys Val Ser Ala Glu Ile Lys Asn Asp			
290	295	300	
Leu Phe Ser Lys Ser Thr Val Gly Leu Gln Cys Leu Arg Ser Asp Ser			
305	310	315	320
Lys Glu Gly Pro Tyr Val Ser Val Pro Leu Asn Cys Ser Cys Gly Asp			
325	330	335	

Thr Val Gln Ala Gln Leu His Asn Leu Glu Pro Cys Met Tyr Val Ala
 340 345 350
 Val Val Ala His Gly Pro Ser Ile Leu Tyr Pro Ser Thr Val Trp Asp
 355 360 365
 Phe Ile Asn Lys Lys Val Thr Val Gly Leu Tyr Gly Pro Lys His Ile
 370 375 380
 His Pro Ser Phe Lys Thr Val Val Thr Ile Phe Gly His Asp Cys Ala
 385 390 395 400
 Pro Lys Thr Leu Leu Val Ser Glu Val Thr Arg Gln Ala Pro Asn Pro
 405 410 415
 Ala Pro Val Ala Leu Gln Leu Trp Gly Lys His Gln Phe Val Leu Ser
 420 425 430
 Arg Pro Gln Asp Leu Lys Val Cys Met Phe Ser Asn Met Thr Asn Tyr
 435 440 445
 Glu Val Lys Ala Ser Glu Gln Ala Lys Val Val Arg Gly Phe Gln Leu
 450 455 460
 Lys Leu Gly Lys Val Ser Arg Leu Ile Phe Pro Ile Thr Ser Gln Asn
 465 470 475 480
 Pro Asn Glu Leu Ser Asp Phe Thr Leu Arg Val Gln Val Lys Asp Asp
 485 490 495
 Gln Glu Ala Ile Leu Thr Gln Phe Cys Val Gln Thr Pro Gln Pro Pro
 500 505 510
 Pro Lys Ser Ala Ile Lys Pro Ser Gly Gln Arg Arg Phe Leu Lys Lys
 515 520 525
 Asn Glu Val Gly Lys Ile Ile Leu Ser Pro Phe Ala Thr Thr Thr Lys
 530 535 540

Tyr Pro Thr Phe Gln Asp Arg Pro Val Ser Ser Leu Lys Phe Gly Lys

545 550 555 560

Leu Leu Lys Thr Val Val Arg Gln Asn Lys Asn His Tyr Leu Leu Glu

565 570 575

Tyr Lys Lys Gly Asp Gly Ile Ala Leu Leu Ser Glu Glu Arg Val Arg

580 585 590

Leu Arg Gly Gln Leu Trp Thr Lys Glu Trp Tyr Ile Gly Tyr Tyr Gln

595 600 605

Gly Arg Val Gly Leu Val His Thr Lys Asn Val Leu Val Val Gly Arg

610 615 620

Ala Arg Pro Ser Leu Cys Ser Gly Pro Glu Leu Ser Thr Ser Val Leu

625 630 635 640

Leu Glu Gln Ile Leu Arg Pro Cys Lys Phe Leu Thr Tyr Ile Tyr Ala

645 650 655

Ser Val Arg Thr Leu Leu Met Glu Asn Ile Ser Ser Trp Arg Ser Phe

660 665 670

Ala Asp Ala Leu Gly Tyr Val Asn Leu Pro Leu Thr Phe Phe Cys Arg

675 680 685

Ala Glu Leu Asp Ser Glu Pro Glu Arg Val Ala Ser Val Leu Glu Lys

690 695 700

Leu Lys Glu Asp Cys Asn Asn Thr Glu Asn Lys Glu Arg Lys Ser Phe

705 710 715 720

Gln Lys Glu Leu Val Met Ala Leu Leu Lys Met Asp Cys Gln Gly Leu

725 730 735

Val Val Arg Leu Ile Gln Asp Phe Val Leu Leu Thr Thr Ala Val Glu

740 745 750

Val Ala Gln Arg Trp Arg Glu Leu Ala Glu Lys Leu Ala Lys Val Ser

755	760	765	
Lys Gln Gln Met Asp Ala Tyr Glu Ser Pro His Arg Asp Arg Asn Gly			
770	775	780	
Val Val Asp Ser Glu Ala Met Trp Lys Pro Ala Tyr Asp Phe Leu Leu			
785	790	795	800
Thr Trp Ser His Gln Ile Gly Asp Ser Tyr Arg Asp Val Ile Gln Glu			
	805	810	815
Leu His Leu Gly Leu Asp Lys Met Lys Asn Pro Ile Thr Lys Arg Trp			
	820	825	830
Lys His Leu Thr Gly Thr Leu Ile Leu Val Asn Ser Leu Asp Val Leu			
	835	840	845
Arg Ala Ala Ala Phe Ser Pro Ala Asp Gln Asp Asp Phe Val Ile			
850	855	860	

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<212> DNA

<213> Homo sapiens

<220>

<221> CDS

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 gcgggcgccg gc atg tgg ctg tgg gag gac cag ggc ggc ctc ctg ggc cct 171

Met Trp Leu Trp Glu Asp Gln Gly Gly Leu Leu Gly Pro

1

5

10

ttc tcc ttc ctg ctg cta gtg ctg ctg ctg gtg acg cgg agc ccg gtc 219
 Phe Ser Phe Leu Leu Leu Val Leu Leu Leu Val Thr Arg Ser Pro Val
 15 20 25
 aat gcc tgc ctc ctc acc ggc agc ctc ttc gtt cta ctg cgc gtc ttc 267
 Asn Ala Cys Leu Leu Thr Gly Ser Leu Phe Val Leu Leu Arg Val Phe
 30 35 40 45
 agc ttt gag ccg gtg ccc tct tgc agg gcc ctg cag gtg ctc aag ccc 315
 Ser Phe Glu Pro Val Pro Ser Cys Arg Ala Leu Gln Val Leu Lys Pro
 50 55 60
 cgg gac cgc att tct gcc atc gcc cac cgt ggc ggc agc cac gac gcg 363
 Arg Asp Arg Ile Ser Ala Ile Ala His Arg Gly Gly Ser His Asp Ala
 65 70 75
 ccc gag aac acg ctg gcg gcc att cgg cag gca gct aag aat gga gca 411
 Pro Glu Asn Thr Leu Ala Ala Ile Arg Gln Ala Ala Lys Asn Gly Ala
 80 85 90
 aca ggc gtg gag ttg gac att gag ttt act tct gac ggg att cct gtc 459
 Thr Gly Val Glu Leu Asp Ile Glu Phe Thr Ser Asp Gly Ile Pro Val
 95 100 105
 tta atg cac gat aac aca gta gat agg acg act gat ggg act ggg cga 507
 Leu Met His Asp Asn Thr Val Asp Arg Thr Thr Asp Gly Thr Gly Arg
 110 115 120 125
 ttg tgt gat ttg aca ttt gaa caa att agg aag ctg aat cct gca gca 555
 Leu Cys Asp Leu Thr Phe Glu Gln Ile Arg Lys Leu Asn Pro Ala Ala
 130 135 140
 aac cac aga ctc agg aat gat ttc cct gat gaa aag atc cct acc cta 603
 Asn His Arg Leu Arg Asn Asp Phe Pro Asp Glu Lys Ile Pro Thr Leu

145	150	155	
agg gaa gct gtt gca gag tgc cta aac cat aac ctc aca atc ttc ttt			651
Arg Glu Ala Val Ala Glu Cys Leu Asn His Asn Leu Thr Ile Phe Phe			
160	165	170	
gat gtc aaa ggc cat gca cac aag gct act gag gct cta aag aaa atg			699
Asp Val Lys Gly His Ala His Lys Ala Thr Glu Ala Leu Lys Lys Met			
175	180	185	
tat atg gaa ttt cct caa ctg tat aat aat agt gtg gtc tgt tct ttc			747
Tyr Met Glu Phe Pro Gln Leu Tyr Asn Asn Ser Val Val Cys Ser Phe			
190	195	200	205
ttg cca gaa gtt atc tac aag atg aga caa aca gat cgg gat gta ata			795
Leu Pro Glu Val Ile Tyr Lys Met Arg Gln Thr Asp Arg Asp Val Ile			
210	215	220	
aca gca tta act cac aga cct tgg agc cta agc cat aca gga gat ggg			843
Thr Ala Leu Thr His Arg Pro Trp Ser Leu Ser His Thr Gly Asp Gly			
225	230	235	
aaa cca cgc tat gat act ttc tgg aaa cat ttt ata ttt gtt atg atg			891
Lys Pro Arg Tyr Asp Thr Phe Trp Lys His Phe Ile Phe Val Met Met			
240	245	250	
gac att ttg ctc gat tgg agc atg cat aat atc ttg tgg tac ctg tgt			939
Asp Ile Leu Leu Asp Trp Ser Met His Asn Ile Leu Trp Tyr Leu Cys			
255	260	265	
gga att tca gct ttc ctc atg caa aag gat ttt gta tcc ccg gcc tac			987
Gly Ile Ser Ala Phe Leu Met Gln Lys Asp Phe Val Ser Pro Ala Tyr			
270	275	280	285
ttg aag aag tgg tca gct aaa gga atc cag gtt gtt ggt tgg act gtt			1035
Leu Lys Lys Trp Ser Ala Lys Gly Ile Gln Val Val Gly Trp Thr Val			

290	295	300	
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Asn Thr Phe Asp Glu Lys Ser Tyr Tyr Glu Ser His Leu Gly Ser Ser			
305	310	315	
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Tyr Ile Thr Asp Ser Met Val Glu Asp Cys Glu Pro His Phe			
320	325	330	
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tcaaaatacc ctttgtgcta gccagggccc tggggaatca ggtgactcac acaaatgcaa			1245
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gagccctgc cctgccctag ctgaggcaca caggagacc cagtaggat aagcacagat			1425
tgaattglac agtttgcaga tgcagatgta aatgcatggg acatgcatga taactcagag			1485
ttgacatttt aaaacttgcc acacttattt caaatatttg tactcagcta tgttaacatg			1545
tactgtagac atcaaacttg tggccatact aataaaatta ttaaaaggag cactaaagga			1605
aaactgtgtg ccaagcatca taicctaagg catacggat ttggggaagc caccatgcaa			1665
tccagtgagg cttcagtgtg cagcaaccaa aatggtaggg aggtcttgaa gccaatgagg			1725
gatttatagc atcttgaata gagagctgca aaccaccagg gggcagagtt gcatttttcc			1785
aggcttttta ggaagctctg caacagatgt gatctgatca taggcaatta gaactggaag			1845
aaacttccaa aaatatctag gtttgtctc attttacaaa tgaggaaact aaactctgtg			1905
gaagggaagg ggttgccica aaagtcacag cttagctggg cacagtggct catgccgata			1965
atcccagcaa ttcagaaagc tgaggcagga ggattacttg aggccagact gggcaatata			2025
gcaagacccc atctctaaaa aattaggcat ggtgtgtcat gcctgtattc ccagctactc			2085
aggaggttga ggtgggagga tcacttgagc ccagaagttc aaggctgcaa tgagccaiga			2145
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<211> 331

<212> PRT

<213> Homo sapiens

<400> 154

Met Trp Leu Trp Glu Asp Gln Gly Gly Leu Leu Gly Pro Phe Ser Phe

1 5 10 15

Leu Leu Leu Val Leu Leu Leu Val Thr Arg Ser Pro Val Asn Ala Cys

20 25 30

Leu Leu Thr Gly Ser Leu Phe Val Leu Leu Arg Val Phe Ser Phe Glu

35 40 45

Pro Val Pro Ser Cys Arg Ala Leu Gln Val Leu Lys Pro Arg Asp Arg

50 55 60

Ile Ser Ala Ile Ala His Arg Gly Gly Ser His Asp Ala Pro Glu Asn

65 70 75 80

Thr Leu Ala Ala Ile Arg Gln Ala Ala Lys Asn Gly Ala Thr Gly Val

85 90 95

Glu Leu Asp Ile Glu Phe Thr Ser Asp Gly Ile Pro Val Leu Met His

100 105 110

Asp Asn Thr Val Asp Arg Thr Thr Asp Gly Thr Gly Arg Leu Cys Asp

115 120 125

Leu Thr Phe Glu Gln Ile Arg Lys Leu Asn Pro Ala Ala Asn His Arg

130 135 140

Leu Arg Asn Asp Phe Pro Asp Glu Lys Ile Pro Thr Leu Arg Glu Ala

145 150 155 160

Val Ala Glu Cys Leu Asn His Asn Leu Thr Ile Phe Phe Asp Val Lys

165 170 175

Gly His Ala His Lys Ala Thr Glu Ala Leu Lys Lys Met Tyr Met Glu

180

185

190

Phe Pro Gln Leu Tyr Asn Asn Ser Val Val Cys Ser Phe Leu Pro Glu

195

200

205

Val Ile Tyr Lys Met Arg Gln Thr Asp Arg Asp Val Ile Thr Ala Leu

210

215

220

Thr His Arg Pro Trp Ser Leu Ser His Thr Gly Asp Gly Lys Pro Arg

225

230

235

240

Tyr Asp Thr Phe Trp Lys His Phe Ile Phe Val Met Met Asp Ile Leu

245

250

255

Leu Asp Trp Ser Met His Asn Ile Leu Trp Tyr Leu Cys Gly Ile Ser

260

265

270

Ala Phe Leu Met Gln Lys Asp Phe Val Ser Pro Ala Tyr Leu Lys Lys

275

280

285

Trp Ser Ala Lys Gly Ile Gln Val Val Gly Trp Thr Val Asn Thr Phe

290

295

300

Asp Glu Lys Ser Tyr Tyr Glu Ser His Leu Gly Ser Ser Tyr Ile Thr

305

310

315

320

Asp Ser Met Val Glu Asp Cys Glu Pro His Phe

325

330

<210> 155

<211> 3377

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (44).. (1666)

<400> 155

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Met Leu Ser Pro

1

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Gln Arg Val Gly Ala Ala Ala Ser Arg Gly Ala Asp Asp Ala Met Glu

5

10

15

20

agc agc aag cct ggt cca gtg cag gtt gtt ttg gtt cag aaa gat caa 151

Ser Ser Lys Pro Gly Pro Val Gln Val Val Leu Val Gln Lys Asp Gln

25

30

35

cat tcc ttt gag cta gat gag aaa gcc ttg gcc agc atc ctc ttg cag 199

His Ser Phe Glu Leu Asp Glu Lys Ala Leu Ala Ser Ile Leu Leu Gln

40

45

50

gac cac atc cga gat ctt gat gtg gtg gtg gtt tca gtg gct ggt gcc 247

Asp His Ile Arg Asp Leu Asp Val Val Val Val Ser Val Ala Gly Ala

55

60

65

ttc cga aag ggc aag tcc ttc att ctg gat ttt atg cta cga tac tta 295

Phe Arg Lys Gly Lys Ser Phe Ile Leu Asp Phe Met Leu Arg Tyr Leu

70

75

80

tat tct cag aag gaa agt ggc cat tca aat tgg ttg ggt gac cca gaa 343

Tyr Ser Gln Lys Glu Ser Gly His Ser Asn Trp Leu Gly Asp Pro Glu

85

90

95

100

gaa ccg tta aca gga ttt tcc tgg aga ggg gga tct gat cca gaa acc 391

Glu Pro Leu Thr Gly Phe Ser Trp Arg Gly Gly Ser Asp Pro Glu Thr

105

110

115

act ggg att caa atc tgg agt gaa gtt ttc act gtg gag aag cca ggt 439

Thr Gly Ile Gln Ile Trp Ser Glu Val Phe Thr Val Glu Lys Pro Gly
 120 125 130
 ggg aag aag gtt gca gtt gtt ctg atg gat acc cag ggg gca ttt gac 487
 Gly Lys Lys Val Ala Val Val Leu Met Asp Thr Gln Gly Ala Phe Asp
 135 140 145
 agc cag tca act gtg aaa gac tgt gct acc atc ttt gct cta agc act 535
 Ser Gln Ser Thr Val Lys Asp Cys Ala Thr Ile Phe Ala Leu Ser Thr
 150 155 160
 atg act agt tct gtt cag att tat aat tta tct cag aac att caa gaa 583
 Met Thr Ser Ser Val Gln Ile Tyr Asn Leu Ser Gln Asn Ile Gln Glu
 165 170 175 180
 gat gat ctt caa cag ctg cag ctc ttc aca gaa tac ggt cgt ctg gca 631
 Asp Asp Leu Gln Gln Leu Gln Leu Phe Thr Glu Tyr Gly Arg Leu Ala
 185 190 195
 atg gat gaa att ttc caa aag cct ttc cag aca ctg atg ttt ttg gtt 679
 Met Asp Glu Ile Phe Gln Lys Pro Phe Gln Thr Leu Met Phe Leu Val
 200 205 210
 aga gat tgg agt ttc cct tat gaa tat agc tat gga ctc caa gga gga 727
 Arg Asp Trp Ser Phe Pro Tyr Glu Tyr Ser Tyr Gly Leu Gln Gly Gly
 215 220 225
 atg gca ttt ttg gat aag cgt tta cag gtg aag gaa cat caa cat gaa 775
 Met Ala Phe Leu Asp Lys Arg Leu Gln Val Lys Glu His Gln His Glu
 230 235 240
 gaa att cag aat gtt cga aat cac att cac tca tgt ttc tcc gat gtc 823
 Glu Ile Gln Asn Val Arg Asn His Ile His Ser Cys Phe Ser Asp Val
 245 250 255 260

acc tgc ttt ctc tta cca cat cca gga ctc cag gtg gcc aca agc cct 871

Thr Cys Phe Leu Leu Pro His Pro Gly Leu Gln Val Ala Thr Ser Pro

265

270

275

gac ttt gat ggg aaa tta aaa gat att gct ggt gaa ttc aaa gag cag 919

Asp Phe Asp Gly Lys Leu Lys Asp Ile Ala Gly Glu Phe Lys Glu Gln

280

285

290

tta cag gca ctg ata ccg tat gta tta aac cca tct aag tta atg gaa 967

Leu Gln Ala Leu Ile Pro Tyr Val Leu Asn Pro Ser Lys Leu Met Glu

295

300

305

aag gag atc aat ggc tca aag gtc acc tgt cgg gga cta ctg gag tat 1015

Lys Glu Ile Asn Gly Ser Lys Val Thr Cys Arg Gly Leu Leu Glu Tyr

310

315

320

ttt aag gca tat att aaa att tat caa gga gaa gat ctg cct cac ccc 1063

Phe Lys Ala Tyr Ile Lys Ile Tyr Gln Gly Glu Asp Leu Pro His Pro

325

330

335

340

aag tcc atg ctt cag gcc act gct gaa gcc aac aac tta gca gct gca 1111

Lys Ser Met Leu Gln Ala Thr Ala Glu Ala Asn Asn Leu Ala Ala Ala

345

350

355

gcc tct gcc aag gac att tat tat aac aac atg gaa gag gtt tgt ggg 1159

Ala Ser Ala Lys Asp Ile Tyr Tyr Asn Asn Met Glu Glu Val Cys Gly

360

365

370

gga gag aaa cct tat ttg tct cca gac att cta gag gag aag cac tgt 1207

Gly Glu Lys Pro Tyr Leu Ser Pro Asp Ile Leu Glu Glu Lys His Cys

375

380

385

gaa ttc aaa caa ctt gct ctg gac cat ttt aag aag acc aag aag atg 1255

Glu Phe Lys Gln Leu Ala Leu Asp His Phe Lys Lys Thr Lys Lys Met

390

395

400

ggt ggg aag gat ttc agc ttt cgt tac cag cag gag ctg gag gag gaa 1303
 Gly Gly Lys Asp Phe Ser Phe Arg Tyr Gln Gln Glu Leu Glu Glu Glu
 405 410 415 420
 atc aag gaa tta tat gag aac ttc tgc aag cac aat ggt agc aag aac 1351
 Ile Lys Glu Leu Tyr Glu Asn Phe Cys Lys His Asn Gly Ser Lys Asn
 425 430 435
 gtc ttc agc acc ttc cga acc cct gca gtg ctg ttc acg ggc att gta 1399
 Val Phe Ser Thr Phe Arg Thr Pro Ala Val Leu Phe Thr Gly Ile Val
 440 445 450
 gct ttg tac ata gcc tca ggc ctc act ggc ttc ata ggt ctt gag gtt 1447
 Ala Leu Tyr Ile Ala Ser Gly Leu Thr Gly Phe Ile Gly Leu Glu Val
 455 460 465
 gla gcc cag ttg ttc aac tgt atg gtt gga cta ctg tta ata gca ctc 1495
 Val Ala Gln Leu Phe Asn Cys Met Val Gly Leu Leu Leu Ile Ala Leu
 470 475 480
 ctc acc tgg ggc tac atc agg tat tct ggt caa tat cgt gag ctg ggc 1543
 Leu Thr Trp Gly Tyr Ile Arg Tyr Ser Gly Gln Tyr Arg Glu Leu Gly
 485 490 495 500
 gga gct att gat ttt ggt gcc gca tat gtg ttg gag cag gct tct tct 1591
 Gly Ala Ile Asp Phe Gly Ala Ala Tyr Val Leu Glu Gln Ala Ser Ser
 505 510 515
 cat atc ggt aat tcc act cag gcc act gtg agg gat gca gtt gtt gga 1639
 His Ile Gly Asn Ser Thr Gln Ala Thr Val Arg Asp Ala Val Val Gly
 520 525 530
 aga cca tcc atg gat aaa aaa gct caa tagcatctta acgtgaagat 1686
 Arg Pro Ser Met Asp Lys Lys Ala Gln

535

540

caaacaagaa cacaacaagc cectactgat ttctgggttt ctgccacggc cacaggttca 1746
tatecagagg aatggcagat ctgagacgat ccaggaagag ctaaaacaig gccctgtaat 1806
aatgagcag acctctcctg tggtttcaaa ttattaaaca cacttccatt tctcttgga 1866
gcatttcttt tecttgcgtt tatagatga agcctgtgtc tattttcata ttactctgt 1926
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<210> 156

<211> 541

<212> PRT

<213> Homo sapiens

<400> 156

Met Leu Ser Pro Gln Arg Val Gly Ala Ala Ala Ser Arg Gly Ala Asp

1 5 10 15

Asp Ala Met Glu Ser Ser Lys Pro Gly Pro Val Gln Val Val Leu Val

20 25 30

Gln Lys Asp Gln His Ser Phe Glu Leu Asp Glu Lys Ala Leu Ala Ser

35 40 45

Ile Leu Leu Gln Asp His Ile Arg Asp Leu Asp Val Val Val Val Ser

50 55 60

Val Ala Gly Ala Phe Arg Lys Gly Lys Ser Phe Ile Leu Asp Phe Met

65 70 75 80

Leu Arg Tyr Leu Tyr Ser Gln Lys Glu Ser Gly His Ser Asn Trp Leu

85 90 95

Gly Asp Pro Glu Glu Pro Leu Thr Gly Phe Ser Trp Arg Gly Gly Ser

100 105 110

Asp Pro Glu Thr Thr Gly Ile Gln Ile Trp Ser Glu Val Phe Thr Val

115 120 125

Glu Lys Pro Gly Gly Lys Lys Val Ala Val Val Leu Met Asp Thr Gln

130 135 140

Gly Ala Phe Asp Ser Gln Ser Thr Val Lys Asp Cys Ala Thr Ile Phe
 145 150 155 160
 Ala Leu Ser Thr Met Thr Ser Ser Val Gln Ile Tyr Asn Leu Ser Gln
 165 170 175
 Asn Ile Gln Glu Asp Asp Leu Gln Gln Leu Gln Leu Phe Thr Glu Tyr
 180 185 190
 Gly Arg Leu Ala Met Asp Glu Ile Phe Gln Lys Pro Phe Gln Thr Leu
 195 200 205
 Met Phe Leu Val Arg Asp Trp Ser Phe Pro Tyr Glu Tyr Ser Tyr Gly
 210 215 220
 Leu Gln Gly Gly Met Ala Phe Leu Asp Lys Arg Leu Gln Val Lys Glu
 225 230 235 240
 His Gln His Glu Glu Ile Gln Asn Val Arg Asn His Ile His Ser Cys
 245 250 255
 Phe Ser Asp Val Thr Cys Phe Leu Leu Pro His Pro Gly Leu Gln Val
 260 265 270
 Ala Thr Ser Pro Asp Phe Asp Gly Lys Leu Lys Asp Ile Ala Gly Glu
 275 280 285
 Phe Lys Glu Gln Leu Gln Ala Leu Ile Pro Tyr Val Leu Asn Pro Ser
 290 295 300
 Lys Leu Met Glu Lys Glu Ile Asn Gly Ser Lys Val Thr Cys Arg Gly
 305 310 315 320
 Leu Leu Glu Tyr Phe Lys Ala Tyr Ile Lys Ile Tyr Gln Gly Glu Asp
 325 330 335
 Leu Pro His Pro Lys Ser Met Leu Gln Ala Thr Ala Glu Ala Asn Asn
 340 345 350

Leu Ala Ala Ala Ala Ser Ala Lys Asp Ile Tyr Tyr Asn Asn Met Glu

355

360

365

Glu Val Cys Gly Gly Glu Lys Pro Tyr Leu Ser Pro Asp Ile Leu Glu

370

375

380

Glu Lys His Cys Glu Phe Lys Gln Leu Ala Leu Asp His Phe Lys Lys

385

390

395

400

Thr Lys Lys Met Gly Gly Lys Asp Phe Ser Phe Arg Tyr Gln Gln Glu

405

410

415

Leu Glu Glu Glu Ile Lys Glu Leu Tyr Glu Asn Phe Cys Lys His Asn

420

425

430

Gly Ser Lys Asn Val Phe Ser Thr Phe Arg Thr Pro Ala Val Leu Phe

435

440

445

Thr Gly Ile Val Ala Leu Tyr Ile Ala Ser Gly Leu Thr Gly Phe Ile

450

455

460

Gly Leu Glu Val Val Ala Gln Leu Phe Asn Cys Met Val Gly Leu Leu

465

470

475

480

Leu Ile Ala Leu Leu Thr Trp Gly Tyr Ile Arg Tyr Ser Gly Gln Tyr

485

490

495

Arg Glu Leu Gly Gly Ala Ile Asp Phe Gly Ala Ala Tyr Val Leu Glu

500

505

510

Gln Ala Ser Ser His Ile Gly Asn Ser Thr Gln Ala Thr Val Arg Asp

515

520

525

Ala Val Val Gly Arg Pro Ser Met Asp Lys Lys Ala Gln

530

535

540

<210> 157

<211> 2172

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (45).. (563)

<400> 157

ggaacacggc acccgcactg cgcgtcatgg tgcaggccctg gtat atg gac gac gcc 56

Met Asp Asp Ala

1

ccg ggc gac ccg cgg caa ccc cac cgc ccc gac ccc ggc cgc cca gtg 104

Pro Gly Asp Pro Arg Gln Pro His Arg Pro Asp Pro Gly Arg Pro Val

5

10

15

20

ggc ctg gag cag ctg cgg cgg ctc ggg gtg ctc tac tgg aag ctg gat 152

Gly Leu Glu Gln Leu Arg Arg Leu Gly Val Leu Tyr Trp Lys Leu Asp

25

30

35

gct gac aaa tat gag aat gat cca gaa tta gaa aag atc cga aga gag 200

Ala Asp Lys Tyr Glu Asn Asp Pro Glu Leu Glu Lys Ile Arg Arg Glu

40

45

50

agg aac tac tcc tgg atg gac atc ata acc ata tgc aaa gat aaa cta 248

Arg Asn Tyr Ser Trp Met Asp Ile Ile Thr Ile Cys Lys Asp Lys Leu

55

60

65

cca aat tat gaa gaa aag att aag atg ttc tac gag gag cat ttg cac 296

Pro Asn Tyr Glu Glu Lys Ile Lys Met Phe Tyr Glu Glu His Leu His

70

75

80

ttg gac gat gag atc cgc tac atc ctg gat ggc agt ggg tac ttc gat 344

Leu Asp Asp Glu Ile Arg Tyr Ile Leu Asp Gly Ser Gly Tyr Phe Asp

85

90

95

100

gtg agg gac aag gag gac cag tgg atc cgg atc ttc atg gag aag gga 392
 Val Arg Asp Lys Glu Asp Gln Trp Ile Arg Ile Phe Met Glu Lys Gly
 105 110 115
 gac atg gtg acg ctc ccc gcg ggg atc tat cac cgc ttc acg gtg gac 440
 Asp Met Val Thr Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Val Asp
 120 125 130
 gag aag aac tac acg aag gcc atg cgg ctg ttt gtg gga gaa ccg gtg 488
 Glu Lys Asn Tyr Thr Lys Ala Met Arg Leu Phe Val Gly Glu Pro Val
 135 140 145
 tgg aca gcg tac aac cgg ccc gct gac cat ttt gaa gcc cgc ggg cag 536
 Trp Thr Ala Tyr Asn Arg Pro Ala Asp His Phe Glu Ala Arg Gly Gln
 150 155 160
 tac gtg aaa ttt ctg gca cag acc gcc tagcagtgtt gcctgggaac 583
 Tyr Val Lys Phe Leu Ala Gln Thr Ala
 165 170
 taacacgtgc ctcgtaaagg tccccaatgt aatgactgag cagaaaatca atcactttct 643
 ctttgcitit agaggatagc cttgaggcta gattatcttt cttttgtaag attatttgat 703
 cagaatattt tgtaatgaaa ggatctagaa agcaacttgg aagtgtaaaag agtcaccttc 763
 attttctgta actcaatcaa gactgggtggg tccatggccc tgtgttagtt catgcattca 823
 gttgagtcce aaatgaaagt ttcattctcc gaaatgcagt tccttagatg cccatctgga 883
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 gaagacactt ttttctccaa aatgatgcct tggggtaggg agtggttaggg ggaagagctc 1003
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 aatttatata tgagctgtgt tagtatitit tcagtgtgag atctctggat tctttcacia 1243

taaagctgtt gaattttaac aggagtatta gtacataaat ttctactca acaattccga 1303
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 gaagggcagg tcgtttttaa agtatttctt tttttaactg gatgaaaaat ctcatgttta 1423
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<210> 158

<211> 173

<212> PRT

<213> Homo sapiens

<400> 158

Met Asp Asp Ala Pro Gly Asp Pro Arg Gln Pro His Arg Pro Asp Pro

1 5 10 15

Gly Arg Pro Val Gly Leu Glu Gln Leu Arg Arg Leu Gly Val Leu Tyr

20 25 30

Trp Lys Leu Asp Ala Asp Lys Tyr Glu Asn Asp Pro Glu Leu Glu Lys

35	40	45	
Ile Arg Arg Glu Arg Asn Tyr Ser Trp Met Asp Ile Ile Thr Ile Cys			
50	55	60	
Lys Asp Lys Leu Pro Asn Tyr Glu Glu Lys Ile Lys Met Phe Tyr Glu			
65	70	75	80
Glu His Leu His Leu Asp Asp Glu Ile Arg Tyr Ile Leu Asp Gly Ser			
85	90	95	
Gly Tyr Phe Asp Val Arg Asp Lys Glu Asp Gln Trp Ile Arg Ile Phe			
100	105	110	
Met Glu Lys Gly Asp Met Val Thr Leu Pro Ala Gly Ile Tyr His Arg			
115	120	125	
Phe Thr Val Asp Glu Lys Asn Tyr Thr Lys Ala Met Arg Leu Phe Val			
130	135	140	
Gly Glu Pro Val Trp Thr Ala Tyr Asn Arg Pro Ala Asp His Phe Glu			
145	150	155	160
Ala Arg Gly Gln Tyr Val Lys Phe Leu Ala Gln Thr Ala			
165	170		

<210> 159

<211> 20

<212> DNA

<220>

<223> Description of the artificial sequence:an artificially synthesized primer sequence

<400> 159

ggaaglgta cttctgctct

20

<210> 160

<211> 50

<212> DNA

<220>

<223> Description of the artificial sequence: an artificially synthesized primer sequence

<400> 160

gagagagaga gagagagaga actagtcctcg agtttttttt tttttttttt 50

<210> 161

<211> 41

<212> DNA

<220>

<223> Description of the artificial sequence: an artificially synthesized primer sequence

<400> 161

gagagagaga gagagagcgg ccgcactagt ccccccccc c 41

<210> 162

<211> 30

<212> RNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence: an artificially synthesized oligo-cap linker sequence

<400> 162

agcaucgagu cggccuuguu ggccuacugg 30

<210> 163

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence: an artificially synthesized oligo(dT) primer sequence

<400> 163

gcggctgaag acggcctatg tggccttttt tttttttttt tt 42

<210> 164
 <211> 21
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of the artificial sequence: an artificially synthesized primer
 sequence
 <400> 164
 agcatcgagt cggccttglt g 21

<210> 165
 <211> 21
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of the artificial sequence: an artificially synthesized primer
 sequence
 <400> 165
 gcggctgaag acggcctatg t 21

<210> 166
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of the artificial sequence: an artificially synthesized primer
 sequence
 <400> 166
 actttattgt catagttag atctatttg 30

<210> 167
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of the artificial sequence: an artificially synthesized primer
 sequence
 <400> 167
 ataatacctta aaaactccat ttccaccct 30

<210> 168
 <211> 1536
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (139).. (1062)
 <400> 168
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 AGCGAAGAGC GGCCTCCTGA GGGAGGGGAA GGGACGTGGG GCGGCCACG GCAGGATTAA 120
 CCTCCATTTC AGCTAATC ATG GGA GAG ATT AAA GTC TCT CCT GAT TAT AAC 171
 Met Gly Glu Ile Lys Val Ser Pro Asp Tyr Asn
 1 5 10

TGG TTT AGA GGT ACA GTT CCC CTT AAA AAG ATT ATT GTG GAT GAT GAT Trp Phe Arg Gly Thr Val Pro Leu Lys Lys Ile Ile Val Asp Asp Asp 15 20 25	219
GAC AGT AAG ATA TGG TCG CTC TAT GAC GCG GGC CCC CGA AGT ATC AGG Asp Ser Lys Ile Trp Ser Leu Tyr Asp Ala Gly Pro Arg Ser Ile Arg 30 35 40	267
TGT CCT CTC ATA TTC CTG CCC CCT GTC AGT GGA ACT GCA GAT GTC TTT Cys Pro Leu Ile Phe Leu Pro Pro Val Ser Gly Thr Ala Asp Val Phe 45 50 55	315
TTC CGG CAG ATT TTG GCT CTG ACT GGA TGG GGT TAC CGG GTT ATC GCT Phe Arg Gln Ile Leu Ala Leu Thr Gly Trp Gly Tyr Arg Val Ile Ala 60 65 70 75	363
TTG CAG TAT CCA GTT TAT TGG GAC CAT CTC GAG TTC TGT GAT GGA TTC Leu Gln Tyr Pro Val Tyr Trp Asp His Leu Glu Phe Cys Asp Gly Phe 80 85 90	411
AGA AAA CTT TTA GAC CAT TTA CAA TTG GAT AAA GTT CAT CTT TTT GGC Arg Lys Leu Leu Asp His Leu Gln Leu Asp Lys Val His Leu Phe Gly 95 100 105	459
GCT TCT TTG GGA GGC TTT TTG GCC CAG AAA TTT GCT GAA TAT ACT CAC Ala Ser Leu Gly Gly Phe Leu Ala Gln Lys Phe Ala Glu Tyr Thr His 110 115 120	507
AAA TCT CCT AGA GTC CAT TCC CTA ATC CTC TGC AAT TCC TTC AGT GAC Lys Ser Pro Arg Val His Ser Leu Ile Leu Cys Asn Ser Phe Ser Asp 125 130 135	555
ACC TCT ATC TTC AAC CAA ACT TGG ACT GCA AAC AGC TTT TGG CTG ATG Thr Ser Ile Phe Asn Gln Thr Trp Thr Ala Asn Ser Phe Trp Leu Met 140 145 150 155	603
CCT GCA TTT ATG CTC AAA AAA ATA GTT CTT GGA AAT TTT TCA TCT GGC Pro Ala Phe Met Leu Lys Lys Ile Val Leu Gly Asn Phe Ser Ser Gly 160 165 170	651
CCG GTG GAC CCT ATG ATG GCT GAT GCC ATT GAT TTC ATG GTA GAC AGG Pro Val Asp Pro Met Met Ala Asp Ala Ile Asp Phe Met Val Asp Arg 175 180 185	699
CTA GAA AGT TTG GGT CAG AGT GAA CTG GCT TCA AGA CTT ACC TTG AAT Leu Glu Ser Leu Gly Gln Ser Glu Leu Ala Ser Arg Leu Thr Leu Asn 190 195 200	747
TGT CAA AAT TCT TAT GTG GTA CCT CAT AAA ATT CGG GAC ATA CCT GTA Cys Gln Asn Ser Tyr Val Val Pro His Lys Ile Arg Asp Ile Pro Val 205 210 215	795

ACT ATT ATG GAT GTG TTT GAT CAG AGT GCG CTT TCA ACT GAA GCT AAA 843
 Thr Ile Met Asp Val Phe Asp Gln Ser Ala Leu Ser Thr Glu Ala Lys
 220 225 230 235
 GAA GAA ATG TAC AAG CTG TAT CCT AAT GCC CGA AGA GCT CAT CTG AAA 891
 Glu Glu Met Tyr Lys Leu Tyr Pro Asn Ala Arg Arg Ala His Leu Lys
 240 245 250
 ACA GGA GGC AAT TTC CCA TAC CTG TGC AGA AGT GCA GAG GTC AAT CTT 939
 Thr Gly Gly Asn Phe Pro Tyr Leu Cys Arg Ser Ala Glu Val Asn Leu
 255 260 265
 TAT GTA CAG ATA CAT TTG CTG CAA TTC CAT GGA ACC AAA TAC GCG GCC 987
 Tyr Val Gln Ile His Leu Leu Gln Phe His Gly Thr Lys Tyr Ala Ala
 270 275 280
 ATT GAC CCA TCA ATG GTC AGT GCC GAG GAG CTT GAG GTG CAG AAA GGC 1035
 Ile Asp Pro Ser Met Val Ser Ala Glu Glu Leu Glu Val Gln Lys Gly
 285 290 295
 AGC CTT GGC ATC AGC CAG GAG GAG CAG TAGTGTGTCT CTCGCTGTCA ATGATGA 1089
 Ser Leu Gly Ile Ser Gln Glu Glu Gln
 300 305
 GTTGACCCGG TGTGTTCTTG TATAGTCAGT GGCATCAGCA CCCGTCAGCC GGCCTTTTCC 1149
 TTCAGGTTTCG TCAGGTCAC CGGTTCTCAC TGTGTCTGGG AAGTAGGACT GATGGTCATC 1209
 TTCATGACAG GCGGCATCTC CACTAAGCCT GTGTAAGTGT TCCCTCTTTG GTTTTCTTAG 1269
 CTTTGAATT TGAAGAAGTA CTTTGAAGA CTCCCATTTT AAGAACCGTG CAGATTTTGC 1329
 TACCAAAAGT CTTCACCACT GTGTTCTTAA GTGAATGTTA ATTTCTGAGG TTTGGGACTT 1389
 TGTGGTGGTT TTTTCTTCT TTTCTTTTCC ATTCTTCTTT CTTTCTTTT ATGTTGTTTG 1449
 CTGTAAATGC TGCACATCCA GATTGCATAT CAGGACATTG GTTATTTTAT GCTTTCTTGG 1509
 ATATAACCAT GATCAGAGTG CCATGGC 1536

<210> 169

<211> 308

<212> PRT

<213> Homo sapiens

<400> 169

Met Gly Glu Ile Lys Val Ser Pro Asp Tyr Asn Trp Phe Arg Gly Thr
 1 5 10 15
 Val Pro Leu Lys Lys Ile Ile Val Asp Asp Asp Ser Lys Ile Trp
 20 25 30
 Ser Leu Tyr Asp Ala Gly Pro Arg Ser Ile Arg Cys Pro Leu Ile Phe
 35 40 45
 Leu Pro Pro Val Ser Gly Thr Ala Asp Val Phe Phe Arg Gln Ile Leu
 50 55 60
 Ala Leu Thr Gly Trp Gly Tyr Arg Val Ile Ala Leu Gln Tyr Pro Val
 65 70 75 80
 Tyr Trp Asp His Leu Glu Phe Cys Asp Gly Phe Arg Lys Leu Leu Asp
 85 90 95
 His Leu Gln Leu Asp Lys Val His Leu Phe Gly Ala Ser Leu Gly Gly
 100 105 110
 Phe Leu Ala Gln Lys Phe Ala Glu Tyr Thr His Lys Ser Pro Arg Val

CGT GAC CGG GTG GGG GTG CAG GAT TTC GTG CTG CTG GAG AAC TTC ACC 375
Arg Asp Arg Val Gly Val Gln Asp Phe Val Leu Leu Glu Asn Phe Thr
45 50 55

AGC GAG GCC GCC TTC ATC GGG AAC CTG CGG CGG CGA TTT CGG GAG AAT Ser Glu Ala Ala Phe Ile Gly Asn Leu Arg Arg Arg Phe Arg Glu Asn 60 65 70	423
CTC ATC TAC ACC TAC ATT GGC CCC GTC CTG GTC TCT GTC AAT CCC TAC Leu Ile Tyr Thr Tyr Ile Gly Pro Val Leu Val Ser Val Asn Pro Tyr 75 80 85 90	471
CGG GAC CTG CAG ATC TAC AGC CGG CAG CAT ATG GAG CGT TAC CGT GGC Arg Asp Leu Gln Ile Tyr Ser Arg Gln His Met Glu Arg Tyr Arg Gly 95 100 105	519
GTC AGC TTC TAT GAA GTG CCC CCT CAC CTG TTT GCC GTG GCG GAC ACT Val Ser Phe Tyr Glu Val Pro Pro His Leu Phe Ala Val Ala Asp Thr 110 115 120	567
GTG TAC CGA GCA CTG CGC ACG GAG CGT CGG GAC CAG GCT GTG ATG ATC Val Tyr Arg Ala Leu Arg Thr Glu Arg Arg Asp Gln Ala Val Met Ile 125 130 135	615
TCT GGG GAG AGC GGG GCA GGC AAG ACC GAG GCC ACC AAG AGG CTG CTG Ser Gly Glu Ser Gly Ala Gly Lys Thr Glu Ala Thr Lys Arg Leu Leu 140 145 150	663
CAG TTC TAT GCA GAG ACC TGC CCA GCC CCC GAG CGC GGA GGT GCC GTG Gln Phe Tyr Ala Glu Thr Cys Pro Ala Pro Glu Arg Gly Gly Ala Val 155 160 165 170	711
CGG GAC CGG CTG CTA CAG AGC AAC CCG GTG CTG GAG GCC TTT GGA AAT Arg Asp Arg Leu Leu Gln Ser Asn Pro Val Leu Glu Ala Phe Gly Asn 175 180 185	759
GCC AAG ACC CTC CGG AAC GAT AAC TCC AGC AGG TTC GGG AAG TAC ATG Ala Lys Thr Leu Arg Asn Asp Asn Ser Ser Arg Phe Gly Lys Tyr Met 190 195 200	807
GAT GTG CAG TTT GAC TTC AAG GGT GCC CCC GTG GGT GGC CAC ATC CTC Asp Val Gln Phe Asp Phe Lys Gly Ala Pro Val Gly Gly His Ile Leu 205 210 215	855
AGT TAC CCC CTG GAA AAG TCA CGA GTG GTG CAC CAG AAT CAT GGG GAG Ser Tyr Pro Leu Glu Lys Ser Arg Val Val His Gln Asn His Gly Glu 220 225 230	903
CGG AAC TTC ACA TCT TCT ACC AGC TGC TGG AGG GGG GCG AGG AGG AGA Arg Asn Phe Thr Ser Ser Thr Ser Cys Trp Arg Gly Ala Arg Arg Arg 235 240 245 250	951
CTC TTC GCA GGC TGG GCT TGG AAC GGA ACC CCC AGA GCT ATC TGT ACC Leu Phe Ala Gly Trp Ala Trp Asn Gly Thr Pro Arg Ala Ile Cys Thr 255 260 265	999
TGG TGAAGGCCAG TGTGCCAAAG TCTTCTTCAT CAACGACAAG AGTGACTGGA AGGTCTG	1058

Trp

TCAGGAAGGC	TCTGACAGTC	ATTGATTTC	CCGAGGATGA	AGTGGAGGAC	CTGCTGAGCA	1118
TCTGAGCCAG	CGTCTTCAT	TTGGGCAACA	TCCACTTTGC	TGCCAACGAG	GAGAGCAATG	1178
CCCAGGTCAC	CACCGAGAAC	CAGCTCAAGT	ATCTGAGCCC	ATTGAGTATG	CGGTGCCTGT	1238
TGTGAAATAC	GACCGCAAGG	GCTACAAGCC	TCGCTCCCGG	CAGCTGCTGC	TCACGCCCAA	1298
CGCCGTCGTC	ATCGTGGAGG	ACGCCAAAGT	CAAGCAGAGG	ATTGATTACG	CCAACCTGAC	1358
CGGAATCTCT	GTCAGCAGCC	TGAGCGACAG	TCTTTTGTG	CTTCATGTAC	AGCGTGCGGA	1418
CAATAAGCAA	AAGGGAGATG	TGGTGCTGCA	GAGTGACCAC	GTGATTGAGA	CGCTGACCAA	1478
GACAGCCCTC	AGTGCCAACC	GCGTGAACAG	CATCAACATC	AACCAGGGCA	GCATCACGTT	1538
TGCAGGGGGC	CCCGGCAGGG	ATGGCACCAT	TGACTTCACA	CCCGGCTCGG	AGCTGCTCAT	1598
CACCAAGGCC	AAGAACGGGC	ACCTGGCTGT	GGTCGCCCCA	CGGCTGAATT	CTCGGTGATA	1658
AAGGCGCCCA	CTGGACCCTC	CCAACGCCCA	ATGCTTTGCT	TTTCTCCTCC	TCCCCTTCCC	1718
AGTTACCAAA	GACTCGAACT	TCCAGACAGG	GACCCAGGGA	CACCCCGAAG	CCCACCTGCA	1778
ATCTCCCACC	TCCTGCCCAT	CCCTCTCTTG	AGGGAGCAGC	AGGGGCCAGG	AGCTACCCCA	1838
GGAGTGGGCC	AGGCCGGGCC	ACAGCAATAG	GAAAGCCAGG	GCCAGAGCGA	GCCATGCCAG	1898
CCCTACTGCC	GATGCCAAAT	ATTTGAGAGA	AGGGAACTTT	TGCTGAGGTT	TTCTCTGAGG	1958
TTTTTTTTGA	TGCTTTATAG	GAACTATTT	TTTAAAAAAA	GCCATTTCCC	ACCCAAGGAC	2018
ACAGTGGATG	TGTTTTCCCT	GACTCCAGCA	GGGCAAGGAA	ATGTAGCCGA	GAGGTTGTGT	2078
GGGCTGGGCT	CTGGTGCCTT	CTTCCCTGGC	CAGGACACCT	CTCCTCCTGA	TTCCCTTGGC	2138
ACCTTGCTCT	TCTGTCTGTT	TACCTGTCTC	CCTGCCTGCC	CATCTGCATC	TTTTGCAGCC	2198
CACTCTGACT	TCCATCTGGG	GGCTGAGACC	ACCCTTGCTT	GCCCCCTTCT	TTCTGCCTTA	2258
AGAATGTCCT	TTTAGGCTGG	GCATGGTGGC	TCACGCCTGT	AACCCAGCA	CTTTGGGAGG	2318
CGGAGACGGG	CAGATAACCT	GAGGTCAGGA	TTTCGAGACC	AACCTGACCT	ACATGGAGAA	2378
ACTCCGCCTC	TGGTAAGGAT	ACAAAATTAG	CCGGGCATGG	TGGTGCACGC	CTCTAATCCC	2438
AGCTGCTCGG	GAGGCTGAGG	CAGGAGAATC	ACTTGAACCC	GGGAAGTGA	GGTTGCAGTG	2498
AGCCAAGAGT	ACACCACTGC	ACTCCAGCCT	GGGCAACAGA	GCGAGACTCC	GTCTTAAAAA	2558
AA						2560

<210> 171

<211> 267

<212> PRT

<213> Homo sapiens

<400> 171

Met	Ala	Leu	Gln	Val	Glu	Leu	Val	Pro	Thr	Gly	Glu	Ile	Ile	Arg	Val
1				5					10					15	
Val	His	Pro	His	Arg	Pro	Cys	Lys	Leu	Ala	Leu	Gly	Ser	Asp	Gly	Val
			20				25						30		
Arg	Val	Thr	Met	Glu	Ser	Ala	Leu	Thr	Ala	Arg	Asp	Arg	Val	Gly	Val
		35				40					45				
Gln	Asp	Phe	Val	Leu	Leu	Glu	Asn	Phe	Thr	Ser	Glu	Ala	Ala	Phe	Ile
	50				55					60					
Gly	Asn	Leu	Arg	Arg	Arg	Phe	Arg	Glu	Asn	Leu	Ile	Tyr	Thr	Tyr	Ile
	65			70				75				80			
Gly	Pro	Val	Leu	Val	Ser	Val	Asn	Pro	Tyr	Arg	Asp	Leu	Gln	Ile	Tyr
			85				90					95			
Ser	Arg	Gln	His	Met	Glu	Arg	Tyr	Arg	Gly	Val	Ser	Phe	Tyr	Glu	Val
		100					105					110			
Pro	Pro	His	Leu	Phe	Ala	Val	Ala	Asp	Thr	Val	Tyr	Arg	Ala	Leu	Arg
		115				120						125			
Thr	Glu	Arg	Arg	Asp	Gln	Ala	Val	Met	Ile	Ser	Gly	Glu	Ser	Gly	Ala
	130				135						140				
Gly	Lys	Thr	Glu	Ala	Thr	Lys	Arg	Leu	Leu	Gln	Phe	Tyr	Ala	Glu	Thr

145		150		155		160									
Cys	Pro	Ala	Pro	Glu	Arg	Gly	Gly	Ala	Val	Arg	Asp	Arg	Leu	Leu	Gln
		165		170		175									
Ser	Asn	Pro	Val	Leu	Glu	Ala	Phe	Gly	Asn	Ala	Lys	Thr	Leu	Arg	Asn
		180		185		190									
Asp	Asn	Ser	Ser	Arg	Phe	Gly	Lys	Tyr	Met	Asp	Val	Gln	Phe	Asp	Phe
		195		200		205									
Lys	Gly	Ala	Pro	Val	Gly	Gly	His	Ile	Leu	Ser	Tyr	Pro	Leu	Glu	Lys
		210		215		220									
Ser	Arg	Val	Val	His	Gln	Asn	His	Gly	Glu	Arg	Asn	Phe	Thr	Ser	Ser
		225		230		235									
Thr	Ser	Cys	Trp	Arg	Gly	Ala	Arg	Arg	Arg	Leu	Phe	Ala	Gly	Trp	Ala
		245		250		255									
Trp	Asn	Gly	Thr	Pro	Arg	Ala	Ile	Cys	Thr	Trp					
		260		265											

<210> 172

<211> 2650

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (116).. (1216)

<400> 172

CTTTTGCTGC TCGCCCCGGG CAGGGGCTGC CGCGGCCCA GGTCCCGCTT CGAGACGCGG 60
 CGCGGTCCAG GCGGGAGGCG ACTCCCTAGG AAGGGACCCG GGGCGGGAGG AGGAA ATG 118
 Met
 1

AGG CCG CGC GGA AGG AAG GCG GCG AGC CCC GGG GCC CCG AGG CCT TGG 166
 Arg Pro Arg Gly Arg Lys Ala Ala Ser Pro Gly Ala Pro Arg Pro Trp
 5 10 15

CCG CGT CAC AGC ACC CAC ATG GCC TCT GGA GTG GGC GCG GCC TTC GAG 214
 Pro Arg His Ser Thr His Met Ala Ser Gly Val Gly Ala Ala Phe Glu
 20 25 30

GAA CTG CCT CAC GAC GGC ACG TGT GAC GAG TGC GAG CCC GAC GAG GCT 262
 Glu Leu Pro His Asp Gly Thr Cys Asp Glu Cys Glu Pro Asp Glu Ala
 35 40 45

CCG GGG GCC GAG GAA GTG TGC CGA GAA TGC GGC TTC TGC TAC TGC CGC 310
 Pro Gly Ala Glu Glu Val Cys Arg Glu Cys Gly Phe Cys Tyr Cys Arg
 50 55 60 65

CGC CAT GCC GAG GCG CAC AGG CAG AAG TTC CTC AGT CAC CAT CTG GCC 358
 Arg His Ala Glu Ala His Arg Gln Lys Phe Leu Ser His His Leu Ala
 70 75 80

GAA TAC GTC CAC GGC TCC CAG GCC TGG ACC CCG CCA GCT GAC GGA GAG 406
 Glu Tyr Val His Gly Ser Gln Ala Trp Thr Pro Pro Ala Asp Gly Glu
 85 90 95

GGG GCG GGG AAG GAA GAA GCG GAG GTC AAG GTG GAG CAG GAG AGG GAG Gly Ala Gly Lys Glu Glu Ala Glu Val Lys Val Glu Gln Glu Arg Glu 100 105 110	454
ATA GAA AGC GAG GCA GGG GAA GAG AGT GAG TCG GAG GAA GAG AGC GAG Ile Glu Ser Glu Ala Gly Glu Glu Ser Glu Ser Glu Glu Glu Ser Glu 115 120 125	502
TCA GAG GAA GAG AGC GAG ACA GAG GAA GAG AGT GAG GAT GAG AGC GAT Ser Glu Glu Glu Ser Glu Thr Glu Glu Glu Ser Glu Asp Glu Ser Asp 130 135 140 145	550
GAG GAG AGT GAA GAA GAC AGC GAG GAA GAA ATG GAG GAT GAG CAA GAA Glu Glu Ser Glu Glu Asp Ser Glu Glu Glu Met Glu Asp Glu Gln Glu 150 155 160	598
AGC GAG GCC GAA GAA GAC AAC CAA GAA GAA GGG GAA TCC GAG GCG GAG Ser Glu Ala Glu Glu Asp Asn Gln Glu Glu Gly Glu Ser Glu Ala Glu 165 170 175	646
GGA GAA ACT GAG GCA GAA AGT GAA TTT GAC CCA GAA ATA GAA ATG GAA Gly Glu Thr Glu Ala Glu Ser Glu Phe Asp Pro Glu Ile Glu Met Glu 180 185 190	694
GCA GAG AGA GTG GCC AAG AGG AAG TGT CCG GAC CAT GGG CTT GAT TTG Ala Glu Arg Val Ala Lys Arg Lys Cys Pro Asp His Gly Leu Asp Leu 195 200 205	742
AGT ACC TAT TGC CAG GAA GAT AGG CAG CTC ATC TGT GTC CTG TGT CCA Ser Thr Tyr Cys Gln Glu Asp Arg Gln Leu Ile Cys Val Leu Cys Pro 210 215 220 225	790
GTC ATT GGG GCT CAC CAG GGC CAC CAA CTC TCC ACC CTA GAC GAA GCC Val Ile Gly Ala His Gln Gly His Gln Leu Ser Thr Leu Asp Glu Ala 230 235 240	838
TTT GAA GAA TTA AGA AGC AAA GAC TCA GGT GGA CTG AAG GCC GCT ATG Phe Glu Glu Leu Arg Ser Lys Asp Ser Gly Gly Leu Lys Ala Ala Met 245 250 255	886
ATC GAA TTG GTG GAA AGG TTG AAG TTC AAG AGC TCA GAC CCT AAA GTA Ile Glu Leu Val Glu Arg Leu Lys Phe Lys Ser Ser Asp Pro Lys Val 260 265 270	934
ACT CGG GAC CAA ATG AAG ATG TTT ATA CAG CAG GAA TTT AAG AAA GTT Thr Arg Asp Gln Met Lys Met Phe Ile Gln Gln Glu Phe Lys Lys Val 275 280 285	982
CAG AAA GTG ATT GCT GAT GAG GAG CAG AAG GCC CTT CAT CTA GTG GAC Gln Lys Val Ile Ala Asp Glu Glu Gln Lys Ala Leu His Leu Val Asp 290 295 300 305	1030
ATC CAA GAG GCA ATG GCC ACA GCT CAT GTG ACT GAG ATA CTG GCA GAC	1078

Ile Gln Glu Ala Met Ala Thr Ala His Val Thr Glu Ile Leu Ala Asp
 310 315 320

ATC CAA TCC CAC ATG GAT AGG TTG ATG ACT CAG ATG GCC CAA GCC AAG 1126
 Ile Gln Ser His Met Asp Arg Leu Met Thr Gln Met Ala Gln Ala Lys
 325 330 335

GAA CAA CTT GAT ACC TCT AAT GAA TCA GCT GAG CCA AAG GCA GAG GGC 1174
 Glu Gln Leu Asp Thr Ser Asn Glu Ser Ala Glu Pro Lys Ala Glu Gly
 340 345 350

GAT GAG GAA GGA CCC AGT GGT GCC AGT GAA GAA GAG GAC ACA TGAAGGCTT 1225
 Asp Glu Glu Gly Pro Ser Gly Ala Ser Glu Glu Glu Asp Thr
 355 360 365

GCTACCCCCA GTGGAAAATC ATCCCCTCCC CTTGTGTGTA TGTGACAGCG TGTATGTAAC 1285
 GGCTTCTGAT TTCTGTGAAA GCTGCTCAGC AACAAACGTA CTTCCACCAG ATGTGTCCCC 1345
 AGATCCACAG CAGGCACATA TCTCTCCAAG GGATGACCAG TTTTATGCTT ACTGTGTGCT 1405
 TCTCATCCCC TGGTTGTGGT AGGTCAAGGA AAAGAGCCCC TTTGATCCAC CAGGAGCAAT 1465
 TAAGAAAGGT CCTTCAGGTA ATCCCTCAAT GGCTGCTTTG AACTTACTCA GGAAAGCCAG 1525
 CCCCCATAAT ATTGTATTAC CAAACAGTAT CGCTTTGTGA GGAAGGATCT GGAATAATCT 1585
 TGAAGGGAAG TCAGAGTTTT CTCCCTGCCT ATTAACAAAA ACCCAATTTT GTTCATATTG 1645
 AAGCATGAAA TAAATGAGAG CAAGGTAGGG CCAAATTAAC TCTTGTGGAC AGTCCCTAAA 1705
 AGTCCAGTTC TACATTTGTG AAAATTGTGG TGCCATGAAT TAAGATGGAT GACTGGAAAA 1765
 AGGTGTTGGA GAAAGAGTTA AAGATGAGGA AGAGATATTT TTAGTATATG AAGTTATCCA 1825
 GGACTTGATA TTCATAATTC AGTGCTGTGG AAATGAAAAA AATGATTGAA GAGGTGGAAC 1885
 GGAAATGACC TTAGGGGGAA AAAAAAGGAC CAAAGAAGTC TGATTAAAAG TTGAAATCAG 1945
 TATTTCTGAA TTCAAATTGC TTGAATTTCC AAAATAGTCA GTAAAGGATC TAATAGAACC 2005
 AGAATTATTT GGGTGAATTC TGCAGGTTTT ATGGGCTTGT CACAACGTGA AGGGCTGGAA 2065
 TGTATATTAC CAAATGGGAA TTTCCATTGT AGGTTTTTGC TAGTCCCACC CCCATTTTAG 2125
 CCTAATTTGG CTAAACGCA GTATGGGGAG AATTGTTCCC ATTCCATGTG TTCTGAATTC 2185
 AGCTCATCTC CCAGCATATA GATATATCCT CCTTTAACTC CGACCAGAAC CCTTCTTCCT 2245
 GTGGCACTCC CCACCCATAG ACCTTCAGAT CATCTCCAC ACCCTGGATC TCACTCTCCT 2305
 CTTAGTAACA GAGACACTCC TGAGGTTGGA CTTCCTTGCT TTTCTCTACT TCCAAATCAC 2365
 AATTTCTTAC AACCAAGCTT TGTGCTCCCG AGTAAGCAGG GATGTACTAG GGGAATGTAA 2425
 AACTGCAAAC TTAATAACCT GCATCTTCTT GAAGCATCAG TTTTACTTAC CAAATGGTTT 2485
 AGAGTCATAA GATGACCTAT TTTTATATAA AAGTTATATT ATAGAATAAA ATGTTCATAC 2545
 GCATAGACTG TTAAG 2560

<210> 173

<211> 367

<212> PRT

<213> Homo sapiens

173

Met Arg Pro Arg Gly Arg Lys Ala Ala Ser Pro Gly Ala Pro Arg Pro
 1 5 10 15

Trp Pro Arg His Ser Thr His Met Ala Ser Gly Val Gly Ala Ala Phe
 20 25 30

Glu Glu Leu Pro His Asp Gly Thr Cys Asp Glu Cys Glu Pro Asp Glu
 35 40 45

Ala Pro Gly Ala Glu Glu Val Cys Arg Glu Cys Gly Phe Cys Tyr Cys
 50 55 60

Arg Arg His Ala Glu Ala His Arg Gln Lys Phe Leu Ser His His Leu

65		70		75		80									
Ala	Glu	Tyr	Val	His	Gly	Ser	Gln	Ala	Trp	Thr	Pro	Pro	Ala	Asp	Gly
				85					90					95	
Glu	Gly	Ala	Gly	Lys	Glu	Glu	Ala	Glu	Val	Lys	Val	Glu	Gln	Glu	Arg
			100					105					110		
Glu	Ile	Glu	Ser	Glu	Ala	Gly	Glu	Glu	Ser	Glu	Ser	Glu	Glu	Glu	Ser
	115					120					125				
Glu	Ser	Glu	Glu	Glu	Ser	Glu	Thr	Glu	Glu	Glu	Ser	Glu	Asp	Glu	Ser
	130					135					140				
Asp	Glu	Glu	Ser	Glu	Glu	Asp	Ser	Glu	Glu	Glu	Met	Glu	Asp	Glu	Gln
145					150					155				160	
Glu	Ser	Glu	Ala	Glu	Glu	Asp	Asn	Gln	Glu	Glu	Gly	Glu	Ser	Glu	Ala
			165					170						175	
Glu	Gly	Glu	Thr	Glu	Ala	Glu	Ser	Glu	Phe	Asp	Pro	Glu	Ile	Glu	Met
	180							185					190		
Glu	Ala	Glu	Arg	Val	Ala	Lys	Arg	Lys	Cys	Pro	Asp	His	Gly	Leu	Asp
	195						200					205			
Leu	Ser	Thr	Tyr	Cys	Gln	Glu	Asp	Arg	Gln	Leu	Ile	Cys	Val	Leu	Cys
	210					215					220				
Pro	Val	Ile	Gly	Ala	His	Gln	Gly	His	Gln	Leu	Ser	Thr	Leu	Asp	Glu
225				230						235				240	
Ala	Phe	Glu	Glu	Leu	Arg	Ser	Lys	Asp	Ser	Gly	Gly	Leu	Lys	Ala	Ala
			245					250					255		
Met	Ile	Glu	Leu	Val	Glu	Arg	Leu	Lys	Phe	Lys	Ser	Ser	Asp	Pro	Lys
	260							265					270		
Val	Thr	Arg	Asp	Gln	Met	Lys	Met	Phe	Ile	Gln	Gln	Glu	Phe	Lys	Lys
	275						280					285			
Val	Gln	Lys	Val	Ile	Ala	Asp	Glu	Glu	Gln	Lys	Ala	Leu	His	Leu	Val
	290					295					300				
Asp	Ile	Gln	Glu	Ala	Met	Ala	Thr	Ala	His	Val	Thr	Glu	Ile	Leu	Ala
305				310						315				320	
Asp	Ile	Gln	Ser	His	Met	Asp	Arg	Leu	Met	Thr	Gln	Met	Ala	Gln	Ala
				325						330				335	
Lys	Glu	Gln	Leu	Asp	Thr	Ser	Asn	Glu	Ser	Ala	Glu	Pro	Lys	Ala	Glu
			340					345					350		
Gly	Asp	Glu	Glu	Gly	Pro	Ser	Gly	Ala	Ser	Glu	Glu	Glu	Asp	Thr	
	355						360						365		

<210> 174

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:a synthetic DNA

<400> 174

ttaagcttgc caccatgagc aaccccagcg ccccaccacc a

41

<210> 175

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:a synthetic DNA

<400> 175

gta t c g a t t t a a t t g c g a t c c c c a t c a g 29

176

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:a synthetic DNA

<400> 176

c a c t a c t g t a t g a c a c c a c a t t c 24

<210> 177

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:a synthetic DNA

<400> 177

g a g a t g c t g t t c c a t g c t g g c c t g 24

<210> 178

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:a synthetic DNA

<400> 178

g g a a a g c t c t c c g t g g c t a a c a a g 24

<210> 179

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:a synthetic DNA

<400> 179

c a t a g t c c t t g a c a a g g g t c a c a g 24

<210> 180

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:a synthetic DNA

<400> 180

cccatcaccatcttccaggagc

22

<210> 181

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:a synthetic DNA

<400> 181

ttcaccaccttcttgatgtcatcata

26

INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP00/06840

A. CLASSIFICATION OF SUBJECT MATTER

Int.Cl⁷ C12N15/12, C07K14/435, 16/18, C12P21/02,
C12Q1/68, A61K38/00, 39/395, 48/00, A61P9/10,
G01N33/50, 33/53,

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

Int.Cl⁷ C12N15/11-15/62, C07K14/00-14/825

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

GenBank/EMBL/DDBJ/GeneSeq, SwissProt/PIR/GeneSeq,
BIOSIS (DIALOG), WPI (DIALOG)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO, 99/14327, A2 (GENENTECH, INC.), 25 March, 1999 (25.03.99), especially, PRO246, FIG.26 (Accession No.X28436), FIG.27 (Accession No.Y05286) & AU, 9893121, A & ZA, 9808293, A	2, 4, 11, 12, 36-40, 43, 45, 46
X	WO, 99/14328, A2 (GENENTECH, INC.), 25 March, 1999 (25.03.99), especially, FIGURE 16 (Accession No.X52221), FIGURE 17 (Accession No.Y13351) & ZA, 9808460, A & AU, 9893178, A & EP, 1027434, A2	2, 4, 11, 12, 36-40, 43, 45, 46
X	US, 5942606, A (INCYTE PHARMACEUTICALS, INC.), 24 August, 1999 (24.08.99), especially, SEQ ID NO:2 (Accession No.X87000), SEQ ID NO:1 (Accession No.Y27096) (Family: none)	2, 4, 11, 12, 36-40, 43, 45, 46
P, X	WO, 99/58660, A1 (HUMAN GENOME SCIENCES, INC.), 18 November, 1999 (18.11.99),	2, 4, 11, 12, 36-40, 43,

☒ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:	"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"A" document defining the general state of the art which is not considered to be of particular relevance	"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"E" earlier document but published on or after the international filing date	"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"&" document member of the same patent family
"O" document referring to an oral disclosure, use, exhibition or other means	
"P" document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search
19 December, 2000 (19.12.00)

Date of mailing of the international search report
26 December, 2000 (26.12.00)

Name and mailing address of the ISA/
Japanese Patent Office

Authorized officer

Facsimile No.

Telephone No.

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
	especially, SEQ ID NO:39 (Accession No.Z65278), SEQ ID NO:291 (Accession No.Y76303) & AU, 9938831, A	45, 46
P, X	WO, 00/11015, A1 (ALPHAGENE, INC.), 02 March, 2000 (02.03.00), especially, SEQ ID NO:37 (Accession No.A23441), SEQ ID NO:38 (Accession No.Y94999) & AU, 9957847, A	2, 4, 11, 12, 36-40, 43, 45, 46
P, X	WO, 00/15666, A2 (GENENTECH, INC.), 23 March, 2000 (23.03.00), especially, FIGURE 15 (Accession No.A30052), FIGURE 16 (Accession No.Y88574) & AU, 9958167, A	2, 4, 11, 12, 36-40, 43, 45, 46
A	TOPPER, James N. et al., "Blood flow and vascular gene expression: fluid shear stress as a modulator of endothelial phenotype", Molecular Medicine Today, January, 1999, Volume 5, Number 1, pages 40-46	1, 2, 4-12, 35-50
A	ANDO, Joji et al., "Flow-dependent Regulation of Gene Expression in Vascular Endothelial Cells", Japanese Heart Journal, January, 1996, Volume 37, Number 1, 19-32	1, 2, 4-12, 35-50

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.: 22,33,51,57,66,69,76

because they relate to subject matter not required to be searched by this Authority, namely:

The inventions as set forth in claims 22, 33, 66 and 69 relate to "methods for inhibiting, promoting or controlling cell apoptosis". As stated in the description, these methods are performed for therapy in the human body. Therefore, these inventions pertain to methods for treatment of the human body by therapy. The inventions as set forth in claims 51, 57 and 76 relate to "drug delivery methods for inducing a fused antibody comprising an antibody bonded to a drug into arteriosclerotic focus" which are to be performed in the human body in therapy. Therefore, these inventions pertain to methods for treatment of the human body by therapy.

2. ☐ Claims Nos.:

because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos.:

because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

See extra sheet.

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

The inventions as set forth in claims which relate to the base sequence represented by SEQ ID NO:143 or the amino acid sequence represented by SEQ ID NO:144

Remark on Protest

☐

The additional search fees were accompanied by the applicant's protest.

☐

No protest accompanied the payment of additional search fees.

第I欄1. の続き

薬剤とを結合させた融合抗体を動脈硬化巣へ誘導する「ドラッグデリバリー法」に関するものであり、ヒトを治療する際に体内で実施されるものであるから、人の身体の治療による処置方法に該当する。

第II欄の続き

, 117, 119, 121, 123, 125, 127, 135, 137, 139, 141, 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109で表される塩基配列（若しくは、配列番号144, 146, 148, 150, 152, 154, 156, 158, 169, 171, 173, 112, 114, 118, 120, 122, 124, 126, 128, 136, 138, 140, 142, 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110で表されるアミノ酸配列）、又は、配列番号115, 116, 129, 130, 131, 132, 133, 134で表される塩基配列、のそれぞれに関連した発明に共通する事項は、「血管内皮細胞においてずり応力刺激により発現が誘導されるDNA」ということである。しかしながら、「血管内皮細胞においてずり応力刺激により発現が誘導されるDNA」としては、出願人も認識しているように endothelin-1 や monocyte chemotactic protein-1 などが既に公知であったから、請求の範囲に記載された上記各塩基配列（又は、アミノ酸配列）に関連した発明に共通する「特別な技術的特徴」は存在しないといえる。

したがって、請求の範囲には、配列番号143, 145, 147, 149, 151, 153, 155, 157, 168, 170, 172, 111, 113, 117, 119, 121, 123, 125, 127, 135, 137, 139, 141, 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109で表される塩基配列（若しくは、配列番号144, 146, 148, 150, 152, 154, 156, 158, 169, 171, 173, 112, 114, 118, 120, 122, 124, 126, 128, 136, 138, 140, 142, 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110で表されるアミノ酸配列）、又は、配列番号115, 116, 129, 130, 131, 132, 133, 134で表される塩基配列、のそれぞれに関連した別異の86発明が包含されている。

Continuation of Box No.II of continuation of first sheet(1)

The requirement of unity of invention in international application (PCT Rule 13.1) is not satisfied unless there is a technical relationship between a group of inventions as set forth in claims involving one or more of the same or corresponding special technical feature. The term "special technical feature" means a technical feature clearly showing the contribution achieved by the inventions as set forth in the claims as a whole (PCT Rule 13.2). The requirement of unity of invention is judged without considering whether the group of inventions are described in separate claims or in a single claim in the alternative form (PCT Rule 13.3).

In the present case, the inventions relating to the base sequences represented by SEQ ID NOS: 143, 145, 147, 149, 151, 153, 155, 157, 168, 170, 172, 111, 113, 117, 119, 121, 123, 125, 127, 135, 137, 139, 141, 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107 and 109 (or the amino acid sequences represented by SEQ ID NOS: 144, 146, 148, 150, 152, 154, 156, 158, 169, 171, 173, 112, 114, 118, 120, 122, 124, 126, 128, 136, 138, 140, 142, 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108 and 110) or the base sequences represented by SEQ ID NO: 115, 116, 129, 130, 131, 132, 133 and 134 have a matter in common "DNA the expression of which is induced by a shear stress stimulus in hemoendothelial cells". However, there had been publicly known endothelin-1, monocyte chemotactic protein-1, etc. as "DNA the expression of which is induced by a shear stress stimulus in hemoendothelial cells", as the applicant recognizes. Therefore, it can be concluded that there is no "special technical feature" common to the inventions relating to the above-described base sequences (or amino acid sequences) as set forth in the claims.

Such being the case, the claims involve 86 separate inventions respectively relating to the base sequences represented by SEQ ID NOS: 143, 145, 147, 149, 151, 153, 155, 157, 168, 170, 172, 111, 113, 117, 119, 121, 123, 125, 127, 135, 137, 139, 141, 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107 and 109 (or the amino acid sequences represented by SEQ ID NOS: 144, 146, 148, 150, 152, 154, 156, 158, 169, 171, 173, 112, 114, 118, 120, 122, 124, 126, 128, 136, 138, 140, 142, 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108 and 110) or the base sequences represented by SEQ ID NO: 115, 116, 129, 130, 131, 132, 133 and 134.

A. 発明の属する分野の分類 (国際特許分類 (IPC))

Int. Cl⁷ C12N15/12, C07K14/435, 16/18, C12P21/02,
C12Q1/68, A61K38/00, 39/395, 48/00, A61P9/10,
G01N33/50, 33/53,

B. 調査を行った分野

調査を行った最小限資料 (国際特許分類 (IPC))

Int. Cl⁷ C12N15/11-15/62, C07K14/00-14/825

最小限資料以外の資料で調査を行った分野に含まれるもの

国際調査で使用した電子データベース (データベースの名称、調査に使用した用語)

GenBank/EMBL/DDBJ/GeneSeq, SwissProt/PIR/GeneSeq,
BIOSIS (DIALOG), WPI (DIALOG)

C. 関連すると認められる文献

引用文献の カテゴリー*	引用文献名 及び一部の箇所が関連するときは、その関連する箇所の表示	関連する 請求の範囲の番号
X	WO, 99/14327, A2 (GENENTECH, INC.) 25.3月.1999 (25.03.99) 特に、PRO246, FIG.26 (Accession No. X28436), FIG.27 (Accession No. Y05286) & AU, 9893121, A & ZA, 9808293, A	2, 4, 11, 12, 36-40, 43, 45, 46
X	WO, 99/14328, A2 (GENENTECH, INC.) 25.3月.1999 (25.03.99) 特に、FIGURE 16 (Accessiion No. X52221),	2, 4, 11, 12, 36-40, 43, 45, 46

☒ C欄の続きにも文献が列挙されている。☐ パテントファミリーに関する別紙を参照。

* 引用文献のカテゴリー

「A」特に関連のある文献ではなく、一般的技術水準を示すもの

「E」国際出願日前の出願または特許であるが、国際出願日以後に公表されたもの

「L」優先権主張に疑義を提起する文献又は他の文献の発行日若しくは他の特別な理由を確立するために引用する文献 (理由を付す)

「O」口頭による開示、使用、展示等に言及する文献

「P」国際出願日前で、かつ優先権の主張の基礎となる出願

の日の後に公表された文献

「T」国際出願日又は優先日後に公表された文献であって出願と矛盾するものではなく、発明の原理又は理論の理解のために引用するもの

「X」特に関連のある文献であって、当該文献のみで発明の新規性又は進歩性がないと考えられるもの

「Y」特に関連のある文献であって、当該文献と他の1以上の文献との、当業者にとって自明である組合せによって進歩性がないと考えられるもの

「&」同一パテントファミリー文献

国際調査を完了した日

19.12.00

国際調査報告の発送日

26.12.00

国際調査機関の名称及びあて先

日本国特許庁 (ISA/JP)

郵便番号100-8915

東京都千代田区霞が関三丁目4番3号

特許庁審査官 (権限のある職員)

内田 俊生

4N

8214

電話番号 03-3581-1101 内線 3488

C (続き) 関連すると認められる文献		
引用文献の カテゴリー*	引用文献名 及び一部の箇所が関連するときは、その関連する箇所の表示	関連する 請求の範囲の番号
	FIGURE 17 (Accession No. Y13351) & ZA, 9808460, A & AU, 9893178, A & EP, 1027434, A2	
X	US, 5942606, A (INCYTE PHARMACEUTICALS, INC.) 24.8月.1999 (24.08.99) 特に、SEQ ID NO:2 (Accession No. X87000), SEQ ID NO:1 (Accession No. Y27096) (ファミリーなし)	2, 4, 11, 12, 36-40, 43, 45, 46
P, X	WO, 99/58660, A1 (HUMAN GENOME SCIENCES, INC.) 18.11月.1999 (18.11.99) 特に、SEQ ID NO:39 (Accession No. Z65278), SEQ ID NO:291 (Accession No. Y76303) & AU, 9938831, A	2, 4, 11, 12, 36-40, 43, 45, 46
P, X	WO, 00/11015, A1 (ALPHAGENE, INC.) 2.3月.2000 (02.03.00) 特に、SEQ ID NO:37 (Accession No. A23441), SEQ ID NO:38 (Accession No. Y94999) & AU, 9957847, A	2, 4, 11, 12, 36-40, 43, 45, 46
P, X	WO, 00/15666, A2 (GENENTECH, INC.) 23.3月.2000 (23.03.00) 特に、FIGURE 15 (Accession No. A30052), FIGURE 16 (Accession No. Y88574) & AU, 9958167, A	2, 4, 11, 12, 36-40, 43, 45, 46
A	TOPPER, James N. et al., "Blood flow and vascular gene ex- pression: fluid shear stress as a modulator of endothelial phenotype", Molecular Medicine Today, January, 1999, Volume 5, Number 1, pages 40-46	1, 2, 4-12, 35-50
A	ANDO, Joji et al., "Flow-dependent Regulation of Gene Ex- pression in Vascular Endothelial Cells", Japanese Heart Journal, January, 1996, Volume 37, Number 1, 19-32	1, 2, 4-12, 35-50

第I欄 請求の範囲の一部の調査ができないときの意見 (第1ページの2の続き)

法第8条第3項 (PCT 17条(2)(a)) の規定により、この国際調査報告は次の理由により請求の範囲の一部について作成しなかった。

1. ☒ 請求の範囲 22, 33, 51, 57, 66, 69, 76 は、この国際調査機関が調査をすることを要しない対象に係るものである。つまり、
請求の範囲 22, 33, 66, 69 の発明は「細胞のアポトーシスを抑制、促進または調節する方法」に関するものであるが、明細書にも記載されているように、これらはヒトの体内で治療を目的として実施されるものであるから、これらの発明は人の身体の治療による処置方法に該当する。また、請求の範囲 51, 57, 76 の発明は、「抗体と
2. ☐ 請求の範囲 _____ は、有意義な国際調査をすることができる程度まで所定の要件を満たしていない国際出願の部分に係るものである。つまり、
3. ☐ 請求の範囲 _____ は、従属請求の範囲であって PCT 規則 6.4(a) の第2文及び第3文の規定に従って記載されていない。

第II欄 発明の単一性が欠如しているときの意見 (第1ページの3の続き)

次に述べるようにこの国際出願に二以上の発明があるとこの国際調査機関は認めた。

国際出願における発明の単一性の要件 (PCT 規則 13.1) は、請求の範囲に記載された一群の発明の間に一又は二以上の同一又は対応する特別な技術的特徴を含む技術的關係があるときに限り、満たされるものであって、この「特別な技術的特徴」とは、請求の範囲に記載された各発明が全体として先行技術に対して行う貢献を明示する技術的特徴のことである (PCT 規則 13.2)。また、発明の単一性の要件の判断は、一群の発明が別個の請求の範囲に記載されているか単一の請求の範囲に択一的な形式によって記載されているかを考慮することなく行われる (PCT 規則 13.3)。

そこで、請求の範囲をみると、請求の範囲に記載された配列番号 143, 145, 147, 149, 151, 153, 155, 157, 168, 170, 172, 111, 113

1. ☐ 出願人が必要な追加調査手数料をすべて期間内に納付したので、この国際調査報告は、すべての調査可能な請求の範囲について作成した。
2. ☐ 追加調査手数料を要求するまでもなく、すべての調査可能な請求の範囲について調査することができたので、追加調査手数料の納付を求めなかった。
3. ☐ 出願人が必要な追加調査手数料を一部のみしか期間内に納付しなかったので、この国際調査報告は、手数料の納付のあった次の請求の範囲のみについて作成した。
4. ☒ 出願人が必要な追加調査手数料を期間内に納付しなかったので、この国際調査報告は、請求の範囲の最初に記載されている発明に係る次の請求の範囲について作成した。

請求の範囲中の配列番号 143 で表される塩基配列又は配列番号 144 で表されるアミノ酸配列に関連した発明

追加調査手数料の異議の申立てに関する注意

- ☐ 追加調査手数料の納付と共に出願人から異議申立てがあった。
☐ 追加調査手数料の納付と共に出願人から異議申立てがなかった。